

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:21 ; Search time 40.04 Seconds
(without alignments)
341.596 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240

Sequence: 1 ETFFPKYHYHDETSKQLLC.....VMHEALHHNYTKSKLSLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Minimum number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_36.*
1: /SIDSL/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /SIDSL/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /SIDSL/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /SIDSL/gcgdata/geneseq/geneseqp/AA1983.DAT.*
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6: /SIDSL/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /SIDSL/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /SIDSL/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /SIDSL/gcgdata/geneseq/geneseqp/AA1988.DAT.*
10: /SIDSL/gcgdata/geneseq/geneseqp/AA1989.DAT.*
11: /SIDSL/gcgdata/geneseq/geneseqp/AA1990.DAT.*
12: /SIDSL/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13: /SIDSL/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14: /SIDSL/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15: /SIDSL/gcgdata/geneseq/geneseqp/AA1994.DAT.*
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17: /SIDSL/gcgdata/geneseq/geneseqp/AA1996.DAT.*
18: /SIDSL/gcgdata/geneseq/geneseqp/AA1997.DAT.*
19: /SIDSL/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /SIDSL/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /SIDSL/gcgdata/geneseq/geneseqp/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1493	66.7	485	13	R24016
2	1488	66.4	518	15	R51003
3	1352	60.4	376	19	W60037
4	1337	59.7	376	18	W50287
5	1332	59.5	438	16	R81882
6	1332	59.5	438	19	W48976
7	1281	57.2	764	21	V68949
8	1256	56.1	963	19	W70540
9	1252.5	55.9	388	19	W73513
10	1252.5	55.9	388	21	W54063
11	1249.5	55.8	664	19	W71603
12	1249.5	55.8	664	21	W80123

13	1249	55.8	445	20	V24153
14	1248.5	55.7	664	19	W71604
15	1248.5	55.7	664	21	W80124
16	1247	55.7	388	19	W73514
17	1247	55.7	388	21	W54064
18	1245.5	55.6	482	19	W31646
19	1245.5	55.6	680	15	W48037
20	1243.5	55.5	449	20	W96278
21	1242	55.4	535	20	W17414
22	1242	55.4	592	20	W70797
23	1242	55.4	592	21	W92185
24	1241.5	55.4	375	18	W06683
25	1241	55.4	595	20	W86003
26	1240.5	55.4	387	17	R90920
27	1239	55.3	399	21	W70867
28	1238.5	55.3	442	18	W10550
29	1238	55.3	396	18	W18574
30	1238	55.3	396	18	W18575
31	1237.5	55.2	784	21	W92207
32	1237	55.2	347	13	R27163
33	1237	55.2	347	21	W83136
34	1237	55.2	400	21	W51523
35	1236	55.2	371	10	P93558
36	1236	55.2	460	21	W69890
37	1236	55.2	480	20	W90205
38	1234.5	55.1	408	21	W44461
39	1234	55.1	329	17	R91806
40	1234	55.1	351	14	R43685
41	1234	55.1	371	10	P91918
42	1234	55.1	446	17	W05829
43	1234	55.1	449	20	W31656
44	1234	55.1	449	14	R43339
45	1234	55.1	449	19	W49816

ALIGNMENTS

RESULT	1
ID	R24016
ID	R24016 standard; Protein: 485 AA.
AC	R24016;
DI	26-NOV-1992 (first entry)
DE	Fusion protein TNFRFc.
XX	
KW	Tumour necrosis factor; TNF; IgG1; immunoglobulin G1.
OS	Synthetic.
XX	
FX	Key
FT	Region
FT	Location/Qualifier
FT	1..252
FT	/note="human TNF extracellular receptor"
FT	Region
FT	253..270
FT	/note="linker and hinge"
FT	Region
FT	271..379
FT	/note="IgG1 CH2"
FT	Region
FT	380..485
FT	/note="IgG1 CH3"
XX	
XX	EP488170-A.
XX	
XX	03-JUN-1992.
PD	
XX	
XX	26-NOV-1991; 91EP-0120187.
XX	
XX	28-NOV-1990; 90DE-4037837.
XX	
XX	(BEHW) BEH:NGWERKE AG.
XX	
XX	Laufer L, Oquendo P, Zettlmeissl G;

Bovine Ix-1 extra
Rat neuritin rece
Rat TNFR alpha and
Human TGFbetaRII:F
Human acid sequenc
Human cytokine rec
tICAM(453)Igc immu
Human noggin/immun
SVPH1-26 disintegr
Human interleukin-
Human IL-6R-alpha-
Heregulin-alpha fu
Anti-5T4 single ch
IL4.Y124D/IgG1 pro
Human interferon-b
Human polypeptide.
Aggrecanase artifi
Aggrecanase artifi
IL-13/IL-4 dual tr
CD2 binding LFA-3-
Human transmembran
Porcine CTLA-4-Ig
Linkered human IgG
Human NR6alpha/IgG
hB7.IgC soluble fu
Human interleukin
Human immunoglobul
Human kappa immuno
Sequence of the 11
Humanised IgD1 ant
Human IgG1 chain C
Completely humanis
Amino acid sequenc

Db	368	nstfrrvsvtlvltlbgdwlngkdykckvksnkalpampgkrlskxakgprepyvltlppard	427
Qy	311	ELTRNNQVSLCLVKGFFPSDIAIVEMSENGCPENNNTKTPVLDSDGSFLLYSKLTVDKSR	370
Db	428	eltnqvslltclvgyfyrlnhaweensngpennyrktltpvldsdgsfllyskltvdksr	487
Qy	371	WQGNFVSCSYMEALHNHYTKSLSPG	400
Db	488	wqgnvfscsymhealnhytqkslslspg	517
RESULT	3		
ID	W60037	standard; Protein; 376 AA.	
AC	W60037;		
XX	11-SEP-1998	(first entry)	
DT			
XX			
XX	Antigenic peptide hFas (nd29) containing Fc region.		
KM	Fas ligand; Fas antagonist; apoptosis related disease; liver disease;		
KM	heart failure; kidney failure; graft-versus-host disease; antibody;		
KM	myocardial infarction; ischemic stenosis; endotoxic shock.		
XX			
OS	Homo sapiens.		
XX			
XX	Key	Location/Qualifiers	
FT	Peptide	1..16	
FT	Protein	/note="hFas antigen signal peptide"	
FT		30..376	
XX		/note="hFas (nd29) protein"	
PN	W09818487-A1.		
PD	07-MAY-1998.		
PF	31-OCT-1997;	97WO-DP03978.	
XX			
XX	26-SEP-1997;	97JP-0262521.	
PR	31-OCT-1996;	96JP-0290459.	
PR	27-DEC-1996;	96JP-0351718.	
XX			
PA	(MOCH) MOCHIDA PHARM CO LTD.		
PA	(OSAB-) OSABA BIOSCIENCE INST.		
PI	Nagata S, Suda T, Yatomi T;		
XX			
XX	WPI: 1998-271925/24.		
XX	N-PSDB: V34430.		
PT	Use of Fas antagonist for treatment and prevention of		
PT	apoptosis-related diseases - such as heart or kidney failure,		
PT	graft-versus-host disease or liver disease		
XX			
PS	Examples; Fig 5-9; 86pp; Japanese.		
XX			
XX	This represents the antigenic peptide hFas (nd29) containing the Fc		
XX	region. The invention provides the use of Fas antagonist as an agent for		
XX	the treatment and prevention of apoptosis-related diseases. The Fas		
XX	antagonist can be a partial Fas antigen peptide containing the		
XX	extracellular part of the protein, but lacking the signal sequence, an		
XX	anti-Fas antibody, or an anti-Fas ligand antibody, where the antibody is		
XX	preferably a humanised antibody. The Fas antagonist is used in the		
XX	treatment and prevention of diseases such as myocardial infarction, heart		
XX	failure, ischemic heart disease, acute kidney failure, graft-versus-host		
XX	disease, ischemic stenosis of the heart, liver or kidney, and		
XX	endotoxic shock, and also as an organ preservative in transplantation.		
XX	The agent is of low toxicity but effectively inhibits the Fas/Fas ligand		
XX	system.		
XX			
Sequence	376 AA:		

Query Match	Similarity	60.4%	Score 1352;	DB 19;	Length 376;
Best Local Similarity	67.3%	Pred. No. 5.5e-78;			
Matches 270;	Conservative 15;	Mismatches 60;	Indels 56;	Gaps	
OY	8	LHYDETSHQLDKDCPQGYLYKHQCIKAW-KTVCAQCPD-HYYDSWHTSDECLYGSFV	65		
DB	23	1hhdgqfch---pcpgerkardctvngdepdcvpcqegkyekldkahfsskerrcr-1	77		
OY	66	CKELAYVQOE--CNTNHRVCECKEGRYLEIEFCLKHNSCP---GEGVQAGTPERMT	119		
DB	78	cdeghglevehactctgntkcrckpfnfctvscv---ehdpcctkcehgllkecltsnt	134		
OY	120	VCKRCPDGFSSNETSSKAPCRKRTKCSVFGLLTKQGNATHDNICSGNSESTQKVDKHT	179		
DB	135	kcka--egsrnsneps-----cdktht	154		
OY	160	CPCPCAPPELLGSPVFTLPKPKKNTLMISRTPEYTCVYVVDVSHEDPEVKFMYVQGVENH	239		
DB	155	cpcpcapell199psvll1pfpkfdclm1stprevcvvvdshedpevfmyvqgvveh	214		
OY	240	NAKTPREEOYSTRVYVSVLTVLHQDMNGEKYCKYSNKALPAPIEKTISKAKGPKE	299		
DB	215	naktprreogynstcyrvsvltvlnqgdlnqdeyckysnkalepalektiskakgqpre	274		
OY	300	POVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIADVEMESNGOPENNYKTTTPVLDSDGSFF	359		
DB	275	pvyvllpsrdektknqysltclvkgfypsdlavewesngqpenyyktltpvldsdgsff	334		
OY	360	LYSKLTVDKSRMQGNGVSCSMHEALNNHYTKSLSPG	400		
DB	335	lyskltvdksrwggnvfscsymhealnnhytqkslslspg	375		
RESULT	4				
W50287					
ID	W50287	standard; Protein; 376 AA.			
AC	W50287;				
XX	XX				
DT	16-JUL-1998	(first entry)			
XX	XX				
DE	Human Fas antigen derivative/IgG1 Fc fusion.				
XX	XX				
KW	Human; Fas antigen; derivative; apoptosis regulation; gene therapy; treatment; diabetes; arthritis; lupus; hepatitis; influenza; HIV; apoptosis modulation; immunoglobulin G1 Fc; IgG1 Fc; fusion.				
KW	XX				
OS	Homo sapiens.				
XX	XX				
FT	Key	Location/Qualifiers			
FT	Peptide	1..16			
FT	Peptide	/label= sig_peptide			
FT	Peptide	17..376			
FT	Peptide	/label= mat_peptide			
XX	XX				
PN	W09742319-A1.				
XX	XX				
PD	13-NOV-1997.				
XX	XX				
PF	01-MAY-1997;	97WO-JP01502.			
XX	XX				
PR	02-MAY-1996;	96JP-0135760.			
XX	XX				
PA	(MOCH) MOCHIDA PHARM CO LTD.				
XX	XX				
PA	(OSAB-) OSAKA BIOSCIENCE INST.				
XX	XX				
PI	Nagata S. Nakamura N;				
XX	XX				
DR	WPI. 1997-558981/51.				
XX	XX				
DR	N-PSDB; V07004.				
XX	XX				

PR Fas antigen derivative containing modified extracellular region -
 PT has low antigenicity, promotes apoptosis and is useful in treatment
 of viral and other diseases

XX Disclousure; Fig 4; 102pp; Japanese.

CC The present sequence is a Fas antigen derivative/IgG1 Fc
 CC fusion, which contains a Fas antigen extracellular region lacking
 CC one or more amino acid residues in the region from the
 CC amino-terminal to (but excluding) the 1st cysteine residue
 CC (preferably at least 29 residues are deleted).

CC The derivative is an effective regulator of apoptosis and can be
 CC used (either by administration of the polypeptide, or by the use
 CC of the coding DNA in gene therapy) to treat a range of diseases,
 CC e.g. diabetes, arthritis, lupus and in particular viral diseases
 CC such as hepatitis, influenza and HIV, by modulating apoptosis of
 CC virus-infected cells.

XX Sequence 376 AA;

Query Match 59.7%; Score 1337; DB 16; Length 376;
 Best Local Similarity 66.6%; Pred. No. 4,8e-77;
 Matches 267; Conservative 16; Mismatches 62; Indels 56; Gaps 9;

QY 8 LHYDETSHOLLCDKCPPTGYLKHCTAKW-KTVCAPCPD-HYTPDSWHTSDECIYCSFV 65

DB 23 lhdqgfcfk-----pcpgerkaridctvngdpcvpcgqegkytdkafskrrcr-1 77

QY 66 CKELOYVKE--CNRTNHNVCCKEGRYLEIEFCLKHNSCRP---GFGVQAGTPERNY 119

DB 78 cdegjglelncitrcnqtkcrckpncfnstvc---ehcdpckcchglkcekltsnt 134

QY 120 VKKRCRDPFNSMTSKACRKHTNCSVGLLLTKGNATHDNICGNSBSOKYDKTHT 179

DB 135 kcke--egsrnsneps-----cckltnt 154

QY 180 CPFCPAPFELLGSPVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVFNMYVDGEVH 239

DB 155 cpcpapelsgpsvflfprkxdtlmisrptevtcvvvdshedpevfnyvdgvevh 214

QY 240 NAKTRPREQYNSTYRVSVLTGLVHODWLNKGEYKCKVSNKALPADIETISKAKQPRE 299

DB 215 naktrpreeqynstyyvsvltglvhdwlnngkyckvsnkalpadietiskakqpre 274

QY 300 POPYTLPRSDLTKNQVSLTGLVGFPSDIAVESNGOENNKTPPVLDSPGSF 359

DB 275 ppytllprsdeltknqvsltclvkgfypsdlavewesngpqnnyktltpvldsgsfi 334

QY 360 IYSKLTVDKSRMOQGVNFCSVNHEALHNHYOKSLSPG 400

DB 335 lysnltvdksrvgqgnvfscsymhealhnhytqkslspg 375

RESULT 5
 ID R81882 standard; Protein; 438 AA.

AC R81882;

DT 30-MAR-1996 (first entry)

XX Plasmid pDC406/OX40/Fc* encoding an OX40/Fc mutein protein.

XX OX40; OX40-L; cytokine; cell surface molecule; plasmid;

KW pDC406/OX40/Fc*; membrane glycoprotein.

XX Synthetic.

XX US5457035-A.

XX 10-OCT-1995.

XX PD

XX

PF 23-JUL-1993; 93US-0097827.

XX 23-JUL-1993; 93US-0097827.

XX (IMMUNEX CORP.

XX Baum PR, Fanslow WC, Gayle RB, Goodwin RG;

XX WPT. 1995-357992/46.

XX N-PSDB; T00829.

XX New isolated DNA encoding the OX40 ligand polypeptide - also vectors

XX and host cells, used to produce recombinant ligand used in e.g.

XX prim. T cell culture, to modulate immune response etc.

XX Example 2; Column 35-38; 26pp; English.

XX This plasmid encodes an OX40/Fc antibody fragment mutein protein,

XX and is used to express a soluble OX40/Fc mutein fusion protein for

XX use in detecting cDNA clones encoding a OX40 ligand. The Fc

XX fragment may be derived from human IgG1, and the plasmid may be

XX used to transform the CV-1/EBNA (ATCC CRL 10478) monkey kidney cell

XX line. Culture supernatant was purified by affinity chromatography

XX and this was used, together with labeled goat anti-human IgG to

XX screen various cell lines.

XX Sequence 438 AA;

Query Match 59.5%; Score 1332; DB 16; Length 438;

Best Local Similarity 62.4%; Pred. No. 1.2e-76;

Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPPTGYLKHCTAKW-KTVCAPCPD-HYTPDSWHTSDECIYCSFV 65

DB 39 cdegjglelncitrcnqtkcrckpncfnstvc---ehcdpckcchglkcekltsnt 134

QY 78 RTHNHNVCCKEGRYLEIEFCLKHNSCRP---GFGVQAGTPERNY 119

DB 97 ptdqdvcr-----pqtprqdsyklvdcvpcpghfs--pqnq 137

QY 138 PCRHTNCSVFGLLTQGNATHDNICGNS-----BST----- 171

DB 138 ackpntnctlsqkqtrhpsdsldavcedrsllatlwtqprftprvtgsltwprts 197

QY 172 -----QKVNKTCTPCPCPAPFELLGSPVFLFPKPKDLMISRTPEVTCVVVDV 220

DB 198 elpstrplveprscckltncpcpaeagarsvllfprkxdtlmisrptevtcvvvdv 257

QY 221 SHEDPEVFNMYVDGEVHNNAKTRPREQYNSTYRVSVLTGLVHODWLNKGEYKCKVSNK 280

DB 258 shedpevfnyvdgvevhnaaktprreeqynstyyvsvltglvhdwlnngkyckvsnk 317

QY 281 ALPADIETISKAKQPREPOVYTLPRSDLTKNQVSLTGLVGFPSDIAVESNGO 340

DB 318 alpadietiskakqprepytllprsdeltknqvsltclvkgfypsdlavewesngq 377

QY 341 PENNYKTPPVLDSPGSFYLISKLTVDKSRMOQGVNFCSVNHEALHNHYOKSLSPG 400

DB 378 pennyktltpvldsgsfiylskltvdksrvgqgnvfscsymhealhnhytqkslspg 437

RESULT 6
 ID W48976 standard; Protein; 438 AA.

AC W48976;

DT 25-SEP-1998 (first entry)

XX OX40/Fc mutein.

XX OX40/Fc; cytokine; T cell antigen; TH-2 immune response; OX40-L;


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XX SO Sequence 764 AA:
Query Match 57.2%; Score 1281; DB 21; Length 764;
Best Local Similarity 59.6%; Pred. No. 3.6e-73;
Matches 270; Conservative 23; Mismatches 66; Indels 94; Gaps 15;

OY 11 DEBTSHOLLCKCPPTGYLKQCTAKMTVCA-----PCPDHY 49
DB 342 dgenyhol-ccp9-ygqchcshlt-cadspcfngscrerngssyacecpnft 396
OY 50 TDSMH-----TSDECLVCPYCKELQYVKQECNRTNHNVCCKEG-----RYLEBEFL 98
DB 397 gsneckvdrctsnpcanng-----gcInrgprstcrprgftgthcelhnsda 446
OY 99 KHRSCPFGVQVQAGT---PERNTVCKRCPDGF-----FSNETSSKAPCRKHTNCSV 147
DB 447 r-spcahg-----gtchdlengpvc-tpagfsggrcevrllthacaagpcfgatc-- 496
OY 148 FGLLLTOKGNATHDNICS-----GN-----SESTOKVDKTHTCPCPCAPE 187
DB 497 -----yglspnntfcncp9yfvgsrcefpvg1ppsfpaaeprkscdkthccpape 550
OY 168 ILGSPVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKRPE 247
DB 551 llgspvflfppkpxdcltmistpevtcvvavshnpemvfmwydgvevmaktkre 610
OY 248 EOYNSTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPQVYTLPP 307
DB 611 eqnastyrvsvltvlhqdwlngkeykckvsnkalpapietiskakgqprepytlpp 670
OY 308 SMDLETKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPVLDSDGSFFLYSKLTVD 367
DB 671 srldetknqvslfclvkvfypsdiavewesngqpennykftrpvldsdgsfflyskltvd 730
OY 368 KSRMOQGNVSCVMHEALHNHYTOKSLSPG 400
DB 731 ksrwqgnvfscsvmhealhnhytqkslspg 763

RESULT 8
W70540 ID W70540 standard; Protein; 963 AA.
AC W70540:

26-JAN-1999 (first entry)

DE Integrin beta-1 chain.
XX Integrin; beta-1 chain; immunoglobulin; chimeric; heterodimer complex;
KW inhibitor; binding; ligand; blood platelet; hemostatic; diagnostic agent;
KM human.
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..20
FT /note= "signal peptide"
FT Protein 21..963
FT /note= "mature protein"
XX
XX W09832771-AL.
XX
XX 30-JUL-1998.
XX
XX 29-JAN-1998; 98W0-JP00370.
XX
XX 29-AUG-1997; 97JP-0234544.
XX
XX 29-JAN-1997; 97JP-0015118.
XX
XX (TORA ) TORAY IND INC.

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XX PI kainoh M, Tanaka T;
XX WP1: 1998-427881/36.
XX DR N-PSDB; V33773.
XX
PT Integrin-immunoglobulin chimeric protein heterodimer complexes as
PT platelet substitutes - contain the alpha and beta integrin chains
PT associated in stable state and bind to extracellular matrix in the
PT presence of plasma components
PS Claim 9; Pages 50-57; 87pp; Japanese.
XX
CC This represents an integrin beta-1 chain. The invention provides
CC integrin-immunoglobulin chimeric protein heterodimer complexes that
CC comprise an integrin alpha or beta chain associated with an
CC immunoglobulin light or heavy chain. These chimeric proteins form
CC heterodimer complexes, in particular with a chimeric protein containing
CC an integrin alpha chain and an immunoglobulin chain with a chimeric
CC protein containing an integrin beta chain and an immunoglobulin chain;
CC the immunoglobulin chain in each case may be a heavy chain, or one of the
CC two may be a light chain. The integrin alpha chain is preferably alpha 4
CC or alpha 2 and the integrin beta chain is preferably beta 1. Animal cells
CC transformed with vectors containing the DNA coding for the above chimeric
CC proteins can be used in the preparation of the chimeric proteins and
CC their heterodimer complexes. The heterodimer complexes, which are useful
CC for testing potential promoters and inhibitors of the binding of
CC integrins to their ligands, function as blood platelet substitutes and
CC hemostatics and as diagnostic agents.
XX
SQ Sequence 963 AA:

Query Match 56.1%; Score 1256; DB 19; Length 963;
Best Local Similarity 51.4%; Pred. No. 1.7e-71;
Matches 272; Conservative 31; Mismatches 90; Indels 136; Gaps 14;

OY 1 ETFPKYIHYDETS--HQLCD-----KCPGR-----YLNQHC 33
DB 441 dsfkrlpigtfeevallqylcececgseglpsbkckneqgtfecagrcnegrvgthc 500
OY 34 TAKWTVCAPCPDHY-----YTDSWHTSDECLVCPYCKELQYVKQ-----EC 76
DB 501 ecstdevnsedmdyrcrtnseelscmngcevcgvrkrdnnehsyqgfcecdnfn 560
OY 77 NETHN-----RYCECKEGRYLEIEFC-LKHNSCP-----GFCVQAGPDER 117
DB 561 drsnqllcgnvgvckrcvcecpnytsacdsldstceasnqgicnrgicecg---- 616
OY 118 NTVCRCRCPDGFSSNMTSSKAP--*-CRKH-----TNCVFGLLLT 153
DB 617 --vck-ctdpxfqtqcemcqlglvcaehkeovqratfnkgekkdtctgecsyfnltkv 673
OY 154 OKGNATHDNI-----CSGNS-----EST 171
DB 674 esrdklpqpvpdpvshckevddcwfyfysvngnnevmhvvenpeoptgpedpeep 733
OY 172 OKVDKTHTCPCPCAPABELIGSPVLEFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNW 231
DB 734 kscdktlhcpcpapelldgspvflfppkrdtmistpevtcvvavshdpdevfnw 793
OY 232 YVDGVEVHNAKTKRPREBOYNSTRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTIS 291
DB 794 yvdgvevhnaktkpreegynstrvsvltvlhqdwlngkeykckvsnkalpapietkis 853
OY 292 KAKGQPREPQVYTLPPSMDLETKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPPV 351
DB 854 kakgqprepytytlppsdeltkqvslfclvkvfypsdiavewesngqpennyktrpv 913
OY 352 LDSGSEFFLYSKLTVDKSRMOQGNVSCVMHEALHNHYTOKSLSPG 400
DB 914 lsdgsfflyskltvdksrwmqgnvfscsvmhealhnhytqkslspg 962

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RESULT 9
ID W73513 standard; Protein: 388 AA.
AC W73513;
XX
XX 02-MAR-1999 (first entry)
DE
DE Rabbit TGFbetaRII:Fc protein.
XX
XX Transforming growth factor-beta receptor; TGF-beta receptor; arthritis;
KM fusion protein; fibroproliferative disorder; diabetic nephropathy;
KM glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
KM collagen vascular disorder; therapy; rabbit.
XX
XX Oryctolagus sp.
OS
OS WO9848024-A1.
PN
PN 29-OCT-1998.
XX
XX 16-APR-1998; 98WO-US07587.
XX
XX 18-APR-1997; 97US-0044641.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Cate R, Gotwals P, Koteliarsky V, Sanicola-Nadel M;
PI
PI WPI: 1998-609994/51.
XX
XX DR N-PSDB: V08998.
XX
XX Transforming growth factor-beta receptor fusion protein - used to
PT treat fibroproliferative disorders
XX
XX Claim 4: Page 18-19; 70pp; English.
XX
XX This sequence is a fusion protein of the rabbit transforming growth
CC factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The
CC encoded protein is an example of a protein of the invention, which are
CC isolated TGF-beta receptor fusion proteins that competitively inhibit
CC binding of TGF-beta to TGF-beta receptor. The fusion protein can be used
CC in a method for lowering the levels of TGF-beta in an individual having
CC arthritis. It can also be used to treat medical conditions such as
CC fibroproliferative disorders. The fibroproliferative disorder is a
CC kidney, intraocular or pulmonary fibrosis, especially selected from
CC diabetic nephropathy, glomerulonephritis, proliferative
CC vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used
CC to treat collagen vascular disorders, including systemic sclerosis,
CC polymyositis, scleroderma, dermatomyositis, and systemic lupus
CC erythematosus. They can also be administered following coronary
CC angioplasty, to prevent restenosis or scarring and reclosing of arteries.
CC
CC Sequence 388 AA:
SO

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Query Match 55.9%; Score 1252.5; DB 19; Length 388;
Best Local Similarity 65.7%; Pred. No. 1e-71;
Matches 257; Conservative 17; Mismatches 70; Indels 47; Gaps 10;

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OY 190 GGFSEVFLPPKPKDRLIMSRPEVTCVVVDSHEDPEVKNFYVDSVEVHNKTKPREQ 249
DB 177 ggpsvllfppkpxdltlmisrpevtcvvdsvedevkfnyvdgvevhnaktkpreeq 236
OY 250 YNSTYRVVSVLAWLHODMNGREKCKVSNKALPAPIETKISKAKQPREPOVYTLPPSR 309
DB 237 ynstyrvvsvlcvlbgdwngkeyckvsnkalpapietkiskakgprepyvyltppsr 296
OY 310 DELTKQVSLTCLVKGFPYSDIAVEMESNGQPPNNYKTPPVLDSDGSFPLYSKLTVDKS 369
DB 297 deltkqvslctclvkgfypsdlavewesngqppennyktppvldsgsfplyskltvdk 356
OY 370 RMOGVNFCQVWHEALNHHYTKSLSPG 400
DB 357 rwqgnvfcswmhealnhytkslispg 387

RESULT 10
ID Y54063 standard; Protein: 388 AA.
AC
AC Y54063;
XX
XX 27-MAR-2000 (first entry)
XX
XX Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.
DE
XX
XX Splice variant; rabbit; transforming growth factor-beta; TGF-beta;
KM type II receptor; Fc portion; human IgG1; fusion protein; arthritis;
KM fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis;
KM diabetic nephropathy; glomerulonephritis; collagen vascular disease;
KM proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;
KM polymyositis; scleroderma; dermatomyositis; systemic lupus erythematosus;
KM restenosis; wound; connective tissue production; adhesion; scarring;
KM post-radiation fibrosis.
XX
XX Synthetic.
OS
OS Oryctolagus cuniculus.
OS
OS Homo sapiens.
XX
XX WO9965948-A1.
XX
XX 23-DEC-1999.
XX
XX 16-JUN-1999; 99WO-US13629.
XX
XX 16-JUN-1998; 98US-0089452.
XX
XX (BIOJ ) BIOGEN INC.
XX
XX Koteliarsky V, Gotwals P, Cate R, Sanicola-Nadel M;
PI
PI WPI: 2000-106083/09.
XX
XX DR N-PSDB: 245251, 245252.
XX
XX New fusion protein of a splice variant of transforming growth
PT factor-beta receptor, for inhibiting the growth factor, e.g. in
PT treatment of fibrosis
XX
XX Disclosure: Page 62-63; 69pp; English.
XX
XX The present sequence represents a splice variant of a rabbit transforming
CC growth factor-beta (TGF-beta) type II receptor fused to the Fc portion
CC of human IgG1. The fusion protein has higher affinity for TGF-beta than
CC fusion proteins comprising the non-variant form of the receptor. The
CC fusion protein contains soluble TGF-beta receptor constructs that are
CC devoid of a transmembrane region (and are secreted from the cell) but
CC retain the ability to bind TGF-beta. The protein competitively inhibits
CC binding of TGF-beta to cellular receptors and/or forms an inactive
CC complex with TGF-beta. The protein is used to reduce levels of TGF-beta,
CC for treatment of arthritic conditions associated with overexpression
CC of TGF-beta, especially fibroproliferative diseases, e.g. renal,
CC intra-ocular or pulmonary fibrosis; diabetic nephropathy;

```

CC glomulonephritis; proliferative vitreoretinopathy; myelofibrosis;
CC collagen vascular disease, e.g. systemic sclerosis, polymyositis;
CC scleroderma, dermatomyositis or systemic lupus erythematosus; and
CC fibrosis associated with restenosis. It is also used for treating
CC wounds, to prevent overproduction of connective tissue and so prevent
CC adhesions or scarring, and to prevent post-radiation fibrosis (by
CC administration to patients about to undergo radiation therapy).

XX Sequence 388 AA;
50

SQ Sequence 388 AA;

Query Match	55.98;	Score 1252.5;	DB 21;	Length 388;
Best Local Similarity	65.78;	Pred No 1a-71;		

Matches 257; Conservative 17; Mismatches 70; Indels 47; Gaps 10;

0y 37 WKTVCAPRBDHYU-----VDSMNTSDE-----CIVC---SPVCKELQYUWCKPCNRTN 81
 17 wtirastlprhvkqsvindmmtvdnngavkfrpqclxfcdvzsrstcdnqgscmsncstl-- 74
 82 RVCECKEGRYLEIEFCLNHRSCRPFGVYAGAPREBRNTVCKRCPD-----GFFSNSTSS 135
 75 sice-----kaheycv-----awrkndentlletcvchdpklayghfllcdsas 148
 0y 135 KAPCKKHTNCVFG---LLLOKGNATHDNICSGNSESTOR---YDKTHTCPPAPAE 169
 119 pkclmkek-kvifgetfmcscstcdcdhllifeeyltsprdlvdkhtcpcpapel 176
 0y 190 GGPVSVEPPPKPKDLMISRTPEYUVCVVVDVSHDEPEKFMWYDGVGEVHNAAKTPREEQ 249
 177 gqpsvflfrpbpkdtdlmistrperetcvvvvdshedpevkfmwydygvemhakkpreeq 256
 0y 250 YNSTYRVVSVLTVLHQDLNMEKEKKCKVSKNALPAPLEKTTISAKGAPREBYOTTLPSR 309
 237 ynstyrvsvlthlvghqdlngkeyckvsknalpalektiskagqpreqvyltlpsr 266
 0y 310 DELTFNQVSLCIVKGFPRSDIAIEMESNQGPENNYKTTTPRVULDSQSFILYSKLTVDKS 369
 237 deltfngvslcivkgyfprsdiaivewesngqpenmykttlrvladsqsfilyskltyvds 356
 0y 370 RMOQGNVFSQSVMEALHNHTOKSLSLSPG 400
 357 twgggnvfscvmeahlmhnyrtqgsislslspg 387

RESULT : 11

W71603 standard; Protein; 664 AA.

W71603;

DT 19-NOV-1998 (first entry)

DE Human neutrin receptor alpha/Fc sequence (Iff2a) fusion protein.

KW Human; neurturin receptor alpha; variant; chimeric;

KW renal; haematological disease.

Synthetic.

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PR 18-FEB-1997;

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PI	Hynes MA, Klein RD, Rosenthal A;
xx	
DR	WPI, 1998-467175/40.
DR	N-PSDB; V58006.
xx	
xx	
PT	New polypeptide(s) based on human neutrinin receptor alpha and
PT	related nucleic acid - useful for increasing survival of
PT	ret-expressing cells for treating e.g. neurological, renal and
PT	haematological diseases

PS · Example 3; Page 81-83; 116pp; English
....

CC The present sequence represents human

CC present/invention. NTNR-alpha proteins can be used: (a) to identify
CC molecules that bind specifically to it (potential agonists and
CC antagonists) and to purify such compounds; (b) to modulate response of
CC cells to neuturin (NTN); (c) to increase survival of Ret-expressing
CC cells or to activate Ret on the surface of cells (soluble glial derived
CC neurotrophic factor receptor (GDNFR alpha) may be used the same way);
CC (d) to increase the half-life of cognate ligands (especially NTN); (e)
CC diagnostically to determine serum levels of its ligands; and (f) as
CC animal feed additive or molecular weight marker. NTNR-alpha, its genes,
CC (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
CC for treating conditions related to abnormal NTN activity or response,
CC particularly neurological (central or enteric), renal or hematopoietic
CC (spleen) diseases or injuries. Ab may be agonists or antagonists for
CC therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-
CC alpha expression, e.g. in some tumours), also reagents for immunoassay
CC and affinity purification.

SQ Sequence 664 AA.

Query Match	Score	DB	Length
55.88;	1249.5;	DB 19;	664;

Matches	264;	Conservative	23;	Mismatches	57;	Indels	71;	Gaps	14;
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0y 32 HCTAAKMKVCAPCP--DH-----YTDSMHTDECELYCSPMCKELOV 72
Db 274 ncrasayqvlts--cpadnygaclsgayagmigtcdmnpnydsapty---lvsapmc----- 322
0y 73 KOECNRTHNRVCECKEGRYLEIEF---CLKH-----RSCP--DGFVGWAQTP 115
Db 324 --scrgsgmeeece--kflr--dfetempclrnaiqatgngvdvnpbkpsfgatgprv 378
0y 116 ERNTYCKRCCKPFGFSSNEISSAKPCRKTHNCVSEFLLLTOKGNMHD-----NICS 165
Db 379 ekt---pslppddlsdstelgstvlctscvsqegsl---kannskelsmefeltcltllp 433
0y 166 GNSSESTGYDTHKPCPCPAPELLGGGSVFLEFPKPKDLMISRTPEVTCVVVDSHEDP 225
Db 432 gprd---pvdkthccpprapelllgsrsvflfppkpxdltmistrpevtccvvdvsnedp 488
0y 226 EYKFNMYVDGVEVHNAKTPREEDYNSTYRVSVLYLVHODMNLGKEYKCKVSKNALPAP 285
Db 489 evkfmydygvevhnaktckpreegynstfyrvsvlylvhqdwlngkeykckvsnkalpap 548
0y 286 IEKTSKAKGPREPQYVYTLPPSSDELTKNVSILCLVKGYPGSDIAVWESNQPEBNY 345
Db 549 laktstkakgprepqvlytlppsseemtknqvsiltclvkgfypsdiaveesngqpeny 608
0y 346 KTTPVLDSDSFFLYSKLTVDKSRMOOGANFSCSVNHEALHNHYTOKSLSLSPG 400
Db 609 ktcpvldsdgsfflysklvtvdksrwqggnfscsvneahlnhytckslslspg 663

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RESULT 12

ID y80123 standard; Protein; 664 AA.

AC Y80123

QY 201 PKDTIMSRPEVTCVVDVSHEDPEVKFNMYVDGVEVHNNAKTRPREQYNSTYRVSVL 260
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 CC 245 PKDTIMSRPEVTCVVDVSHEDPEVKFNMYVDGVEVHNNAKTRPREQYNSTYRVSVL 304
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 261 TVLHODWLNKREYKCKVSNKALPAPIEKTISKAKGPREPOVYTLPSRDELTKNOVSLT 320
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 305 tvlhdqwlngkreykckvsnkalpapiektiskakgprepyytlpsrdeltknqvalt 364
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 321 CLVNGFYSDIAVWESNGOPENNKITPPVLDSDGSFFLYSKLTVDSKRMQGNVFCSS 380
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 365 clvngfydsdlaewesngopennyktlppvldsdgsfflyskltvdksrwtgqgnvfscs 424
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 381 VMHEALHNHYTKRSLSLSPG 400
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 425 vmhealhnhytkrslslspg 444
 CC ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 RESULT 14
 W71604 standard; Protein; 664 AA.
 AC W71604;
 DT 19-NOV-1998 (first entry)
 DE Rat neuturin receptor alpha/Fc sequence (IIF2a) fusion protein.
 XX
 KW Human; neuturin receptor alpha; NTNR-alpha; variant; chimeric;
 KW fusion protein; immunoadhesion; ret-expressing cell; neurological;
 KW renal; haematological disease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS Rattus sp.
 XX
 PN MO9836072-A1.
 XX
 PD 20-AUG-1998.
 XX
 PF 17-FEB-1998; 98MO-US03179.
 XX
 PR 24-OCT-1997; 97US-0957063.
 PR 18-FEB-1997; 97US-0802805.
 PR 09-JUN-1997; 97US-0871913.
 XX
 PA (GETH) GENENTECH INC.
 Hynes MA, Klein RD, Rosenthal A;
 WPI: 1998-467175/40.
 N-PSDB: V58007.
 PT New polypeptide(s) based on human neuturin receptor alpha and
 PT related nucleic acid - useful for increasing survival of
 PT ret-expressing cells for treating e.g. neurological, renal and
 PT haematological diseases
 XX
 PS Example 3; Page 84-86; 116pp; English.
 XX
 CC The present sequence represents rat neuturin receptor alpha
 CC (NTNR-alpha)/Fc sequence (IIF2a) fusion protein, from an example of the
 CC present invention. NTNR-alpha proteins can be used: (a) to identify
 CC molecules that bind specifically to it (potential agonists and
 CC antagonists) and to purify such compounds; (b) to modulate response of
 CC cells to neuturin (NTN); (c) to increase survival of Ret-expressing
 CC cells or to activate Ret on the surface of cells (soluble glial derived
 CC neurotrophic factor receptor (GDNFR alpha) may be used the same way);
 CC (d) to increase the half-life of cognate ligands (especially NTN); (e)
 CC diagnostically to determine serum levels of its ligands; and (f) as
 CC animal feed additive or molecular weight marker. NTNR-alpha, its genes,
 CC (ant)agonists and antisense nucleic acids, are useful in vivo or ex vivo
 CC for treating conditions related to abnormal NTN activity or response,
 CC particularly neurological (central or enteric), renal or haematopoietic

CC (spleen) diseases or injuries. Ab may be agonists or antagonists for
 CC therapeutic use (e.g. as antagonists to treat excessive/unwanted NTNR-
 CC alpha expression, e.g. in some tumours), also reagents for immunoassay
 CC and affinity purification.
 XX
 SO Sequence 664 AA;
 Query Match 55.7%; Score 1248.5; DB 19; Length 664;
 Best Local Similarity 62.7%; Pred. No. 3,4e-71; Indels 73; Gaps 11;
 Matches 261; Conservative 21; Mismatches 61;
 QY 32 HCTAKMKTVCAPCP-DHY-----YDSSWHTSDECLYCSPVCKELQYV 72
 Db 274 ncrasylrits-cpadhygaqlsgyagmifdmtprnydsnptg----lvspwc----- 323
 QY 73 KOECNRTHNRYECKE-----GRYLEFECLKHNSCPGFGVQAGT 114
 Db 324 --ncrgsgmneeceklfirdftempclrnaiaqafngtdvmmpskpslp---atqapr 377
 QY 115 PERNTVCKRCRDPGFFSNFETSSKAPCRKHTNCSYVGLLTOKGNATHD-----NIC 164
 Db 378 vekt---pslpddlsdstslgtsvltctstsqegll---kannskelsmcftaltlnls 430
 QY 165 SGNSESTQKVDKTHTCPPCAPPELLGSPSVFLFPPKPKDTIMSRPEVTCVVDVSHED 224
 Db 431 pg---srdpvkhtntpcpcpapel1lgpsvflfppkpkdtlmisrtpevtcvvdvshed 487
 QY 225 PEVKFNMYVDGVEVHNNAKTRPREQYNSTYRVSVLTVLHODWLNKREYKCKVSNKALPA 284
 Db 488 pevknmyvdgvevhnnaaktkrpreeqynstyrvsvlvtlhdqwlngkreykckvsnkalpa 547
 QY 285 PIEKTISKAKGPREPOVYTLPSRDELTKNOVSLTCLVKGFGYSDIAVWESNGOPENN 344
 Db 548 piektiskakgprepyytlpsrdeltknqvaltclvkgfypsdlavewesngopenn 607
 QY 345 YKTPPVLDSDGSFFLYSKLTVDSKRMQGNVFCSSVMHEALHNHYTKRSLSLSPG 400
 Db 608 yktppvldsdgsfflyskltvdksrwtgqgnvfscsvmhealhnhytkrslslspg 663
 RESULT 15
 Y80124 standard; Protein; 664 AA.
 ID Y80124
 AC Y80124;
 DT 19-MAY-2000 (first entry)
 DE Rat NTNR alpha and Igg fusion protein SEQ ID NO:18.
 XX
 KW Human; neuturin receptor alpha; NTNR alpha; splenic haematopoiesis;
 KW anaemia; Thrombocytopaenia; hypoplasia; haemorrhage.
 XX
 OS Rattus sp.
 OS Synthetic.
 XX
 PN US6025157-A.
 XX
 PD 15-FEB-2000.
 PF 24-OCT-1997; 97US-0957063.
 PR 18-FEB-1997; 97US-0038839.
 PR 09-JUN-1997; 97US-0049818.
 XX
 PA (GETH) GENENTECH INC.
 Hynes MA, Rosenthal A, Klein RD;
 WPI: 2000-181808/16.
 N-PSDB: 291460.
 DR

PT Isolated nucleic acid molecule encodes a neurturin receptor-alpha amino
PT acid sequence excluding the N-terminal signal peptide -

PS Claim 3; Column 97-102; 78pp; English.

XX The present invention describes a neurturin receptor alpha (NTR alpha).
CC NTR alpha binds neurturin. The NTR alpha nucleic acid molecule is
CC useful for the expression of NTR alpha, which may be used to identify
CC agonist and antagonist compounds having therapeutic applications, such
CC as enhancing splenic haematopoiesis, treating anaemia,
CC thrombocytopenia, hypoplasia, or haemorrhage. The present sequence
CC is a NTR alpha and 1gc (immunoglobulin G) fusion protein from the
CC present invention.

XX Sequence 664 AA;

Query Match 55.7%; Score 1248.5; DB 21; Length 664;
Best Local Similarity 62.7%; Pred. No. 3.4e-71;
Matches 261; Conservative 21; Mismatches 61; Indels 73; Gaps 11;

32 HCTAKWKTVCAPCP-DHY-----YTDSMHTSDECLXCSPYCKELQYV 72
Db 274 ncrasyrilts-cpadnygcclsgysagmlgfmdtptydsnptg---lvspwc----- 323
QY 73 KOECNTHNRVCKCKE-----GRLEIEFLKHSRCPGFGVVOAGT 114
Db 324 --ncrgsgmeeceekfldfienplnaidqafngtdvmspkgpslp---atqapr 377
QY 115 PERNTYCKRCRCPDGFSENETSSKAPCRKHTNCSVFGLLTQGNATHD-----NIC 164
Db 378 vekt---pslpddlsdstsgtstictctsgl---kannskelmscfeiltntis 430
QY 165 SGNSESTOKVDTHTCTPCPAPPELLGSPVFLPPPKRDTLMISRPPEVTCVYVDVSHED 224
Db 431 pg---srpvdktctcpopapellgspvflfpkpcktlmsrptevtcvvdvshd 487
QY 225 PEYKFWYVDGVVHNAKTPREDOYNSTRVSVLTVLHODWLNKREYCKVSNKALPA 284
Db 488 pevkinwydvgevhnaktpreeqynstyrvsvltvlhqdwlngkeyckvsnkalpa 547
QY 285 PIKRTISKAKGPREPOVYTLPPSRDELTKNOYSLNCLVKGFPSPDIAYEMESNGOPENN 344
Db 548 plektiskakgprepqvylfppsrdeemckngvsltelvkgfypsdlavewesngqpen 607
QY 345 YKTPPVLDSDGSFFLYSKLTVDKSRMOGNVFSCSYMEALNNHYTOKSLSPG 400
Db 608 yktppvlstdsgsflyskltvdkstrwqgnvfscsymhealnhytrqkslspg 663

Search completed: December 27, 2000, 10:53:25
Job time: 116 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:53 ; Search time 27.53 Seconds

(without alignments)
243.533 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240

Sequence: 1 ETFFPPKYLHDETSHQLLC.....VMHEALHNYTKSLSPG 400

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 1676186 residues

1 number of hits satisfying chosen parameters: 164575

Maximum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA: *
1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep: *
2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep: *
3: /cgn2_6/ptodata/2/1aa/6.COMB.pep: *
4: /cgn2_6/ptodata/2/1aa/PCYUS.COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/backfill1est.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1510.5	67.4	486	1	US-08-243-010-1
2	1502	67.1	518	1	US-08-385-229-4
3	1332	59.5	438	1	US-08-097-827-11
4	1332	59.5	438	1	US-08-494-574-11
5	1266.5	56.5	911	2	US-08-484-438-10
6	1249.5	55.8	664	3	US-08-957-063-16
7	1248.5	55.7	664	3	US-08-957-063-16
8	1243.5	55.5	449	3	US-08-897-236-23
9	1240.5	55.4	387	1	US-08-470-299-4
10	1238.5	55.3	442	4	PCT-US96-10043-9
11	1238	55.3	396	2	US-08-784-512-3
12	1237	55.2	347	1	US-07-940-861-43
13	1237	55.2	347	1	US-08-459-512-43
14	1237	55.2	347	2	US-08-459-657-43
15	1237	55.2	347	2	US-08-460-132-43
16	1237	55.2	347	4	PCT-US92-02050-43
17	1234	55.1	371	1	US-08-236-311-7
18	1234	55.1	371	1	US-08-457-918-7
19	1234	55.1	449	1	US-08-458-516-13
20	1234	55.1	459	1	US-08-157-101A-7
21	1234	55.1	476	2	US-08-378-939-10
22	1234	55.1	476	3	US-08-487-550-4
23	1234	55.1	476	3	US-08-487-550-12
24	1234	55.1	478	3	US-08-487-550-8
25	1228	54.8	232	2	US-08-593-043A-50
26	1228	54.8	254	2	US-08-284-391B-33
27	1228	54.8	424	4	PCT-US95-03866-12
28	1228	54.8	424	4	PCT-US95-03866-14

29	1228	54.8	437	4	PCT-US96-10043-11	Sequence 11, Appl
30	1228	54.8	451	2	US-08-887-352B-14	Sequence 14, Appl
31	1228	54.8	451	2	US-08-887-352B-16	Sequence 16, Appl
32	1228	54.8	451	2	US-08-887-352B-18	Sequence 18, Appl
33	1228	54.8	451	3	US-08-466-151-65	Sequence 65, Appl
34	1228	54.8	452	3	US-09-027-449-71	Sequence 71, Appl
35	1228	54.8	453	3	US-08-466-151-8	Sequence 8, Appl
36	1228	54.8	454	2	US-07-934-373C-22	Sequence 22, Appl
37	1228	54.8	454	3	US-08-437-642B-22	Sequence 22, Appl
38	1228	54.8	454	4	PCT-US93-07832-22	Sequence 22, Appl
39	1226.5	54.8	442	1	US-08-461-968A-5	Sequence 5, Appl
40	1226.5	54.8	442	2	US-08-462-571-5	Sequence 5, Appl
41	1217.5	54.4	552	1	US-08-243-010-6	Sequence 6, Appl
42	1207	53.9	232	1	US-07-797-556-4	Sequence 4, Appl
43	1207	53.9	232	1	US-08-225-889-4	Sequence 4, Appl
44	1207	53.9	232	1	US-08-570-623-4	Sequence 4, Appl
45	1207	53.9	232	4	PCT-US95-06530-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-243-010-1
Sequence 1, Application US/08243010
Patent No. 5639597
GENERAL INFORMATION:
APPLICANT: Lafifer, Leander
APPLICANT: Zettlmeissel, Gerd
APPLICANT: Oquendo, Patricia
TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
STREET: 1300 I Street, N.W.
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/243,010
FILING DATE: 13-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/798,564
FILING DATE: 26-NOV-1991
APPLICATION NUMBER: DE P 40 37 837.3
FILING DATE: 28-NOV-1990
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 32,220
REFERENCE/DOCKET NUMBER: 02481-1132-00000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 486 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TY.: peptide
US-08-243-010-1
Query Match 67.4%; Score 1510.5; NB 1; Length 486;
Best Local Similarity 65.2%; Pred. No. 1,6e-118;

Matches 292: Conservative 17: Mismatches 76: Indels 63: Gaps 5:

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OY 9 HYDEETSHQLLDCKPPGYTLKQHCIAKKTVCAPCPDHYTDSMTSDECLYCSVPCKE 68
DB 45 YVDQ--TAQMCSSKSPGQHAKECTKTSYDVCSDCEDSTYTQLMNWMVECLSCGSCSS 102
OY 69 LQYVKECNRTHNRVCEKEGRILEI-----EFLKHSRCPGFGVVOAGTPERNYVCK 122
DB 103 DQVETQACTREONRITCTCRPGWYCALSKQEGCRLCAPLKRCPGFGVAVRGTTSDYVCK 162
OY 123 RCPDGFESNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNS----- 168
DB 163 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPO 218
OY 169 -----ESTQKVDKHTCPCPAPELLGGP 192
DB 219 PVSTRSQHTQTPPEPSTABSTFLLPMGSPPAEGSTGDEPKSCDKHTHCPCPAPELLGG 278
OY 193 SVLEFPKPKDITLMISTREPTVCVVDVSHEDPEVKFNMTYVDGEVHNATKPREBOYNS 252
DB 279 SVLEFPKPKDITLMISTREPTVCVVDVSHEDPEVKFNMTYVDGEVHNATKPREBOYNS 338
OY 253 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDEL 312
DB 339 TYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRDEL 397
OY 313 TRKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 372
DB 398 TRKNQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 457
OY 373 QGQNVFSCSVMEALHNHYTKSLSPG 400
DB 458 QGQNVFSCSVMEALHNHYTKSLSPG 485

```

RESULT 2
US-08-385-229-4
Sequence 4, Application US/08385229
Patent No. 5605690
GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:

LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-4

Query Match 67.1%; Score 1502; DB 1; Length 518;
Best Local Similarity 63.8%; Pred. No. 8,9e-118;
Matches 287: Conservative 21: Mismatches 78: Indels 64: Gaps 4:

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OY 9 HYDEETSHQLLDCKPPGYTLKQHCIAKKTVCAPCPDHYTDSMTSDECLYCSVPCKE 68
DB 74 YVDQ--TAQMCSSKSPGQHAKECTKTSYDVCSDCEDSTYTQLMNWMVECLSCGSCSS 131
OY 69 LQYVKECNRTHNRVCEKEGRILEI-----EFLKHSRCPGFGVVOAGTPERNYVCK 122
DB 132 DQVETQACTREONRITCTCRPGWYCALSKQEGCRLCAPLKRCPGFGVAVRGTTSDYVCK 191
OY 123 RCPDGFESNETSSKAPCRKHTNCSVFGLLLTQGNATHDNICSGNS----- 168
DB 192 PCAPGTFSTSTSDICRPHQICNVVAI-----PGNASMDAVCTSTSPTRSMAPGAVHLPO 247
OY 169 -----ESTQKVDKHTCPCPAPELLG 190
DB 248 PVSTRSQHTQTPPEPSTABSTFLLPMGSPPAEGSTGDEPKSCDKHTHCPCPAPELLG 307
OY 191 GRSVLEFPKPKDITLMISTREPTVCVVDVSHEDPEVKFNMTYVDGEVHNATKPREBOY 250
DB 308 GRSVLEFPKPKDITLMISTREPTVCVVDVSHEDPEVKFNMTYVDGEVHNATKPREBOY 367
OY 251 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 310
DB 368 NSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAKGQPREPPQVYTLPPSRD 427
OY 311 ELTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 370
DB 428 ELTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSR 487
OY 371 WOQNVFSCSVMEALHNHYTKSLSPG 400
DB 488 WOQNVFSCSVMEALHNHYTKSLSPG 517

```

RESULT 3
US-08-097-827-11
Sequence 11, Application US/08097827
Patent No. 5457035
GENERAL INFORMATION:
APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Manslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5457035el cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE:
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:

NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-097-827-11

Query Match 59.5%; Score 1332; DB 1; Length 438;
Best Local Similarity 62.4%; Pred. No. 1,1e-103;
Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPGTYLKQCHTAKMKTVCAPCPDHYTID--SMHTSDECLYCSPVCKELQYKQECN 77
39 CRECQPHGKVNRCBHTRDLCHPCETGTFYNEAVNDTCQCTQCNH--RSGSELKQNC 96
78 RTHNRVCECKEGRYLIEIFCLKHSRCPGPGVYQAGTPERNTVCKRCPDGFSENETSKA 137
DB 97 PTDVTCRCR-----PGTPRQDSGYKLGVDVCVCPGCHFS--PGNNQ 137
QY 138 PCCKHNCVFGILLTQKNATHDNICSGNS-----EST----- 171
DB 138 ACKPMTNCTLSGKOTRHPASDSIDAVCEDRSLATILMETQRPRTTVQSTVMPRTS 197
QY 172 -----OKVDTHNCPCPAPPELLGSPVFLFPKPKDTLMSRPEVTCVAVY 220
DB 198 ELPSTTLVEPRKCDTHCPCPAPBAGAPSVFLFPKPKDTLMSRPEVTCVAVY 257
QY 221 SHEDPEVKEVMYDGEVHNAAKTPREEOYNSTYRVSVLTVLHODMLNGKEYCKKVSNK 280
DB 258 SHEDPEVKEVMYDGEVHNAAKTPREEOYNSTYRVSVLTVLHODMLNGKEYCKKVSNK 317
QY 281 ALPAPIEKTISAKKGPPEPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGQ 340
DB 318 ALPAPIEKTISAKKGPPEPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGQ 377
QY 341 PENNYKTPPVLDSDGSFFLYSKLTVDKSRMOOGNVSFCSVMHEALHNHYTOKSLSPG 400
DB 378 PENNYKTPPVLDSDGSFFLYSKLTVDKSRMOOGNVSFCSVMHEALHNHYTOKSLSPG 437

RESULT 4

US-08-494-574-11
Sequence 11, Application US/08494574
Patent No. 5783665

GENERAL INFORMATION:

APPLICANT: Baum, Peter
APPLICANT: Goodwin, Ray
APPLICANT: Fanslow, William
APPLICANT: Gayle, Richard
TITLE OF INVENTION: No. 5783665el Cytokine which is a ligand for
TITLE OF INVENTION: OX40
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: USA

COMPUTER READABLE FORM:

ZIP: 98101
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/494,574

FILING DATE: 22-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/097,827
FILING DATE: 23-JUL-1993
ATTORNEY/AGENT INFORMATION:
NAME: Perkins, Patricia A.
REGISTRATION NUMBER: 34,693
REFERENCE/DOCKET NUMBER: 2806
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-587-0730
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 438 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-494-574-11

Query Match 59.5%; Score 1332; DB 1; Length 438;
Best Local Similarity 62.4%; Pred. No. 1,1e-103;
Matches 262; Conservative 23; Mismatches 75; Indels 60; Gaps 6;

QY 20 CDKCPGTYLKQCHTAKMKTVCAPCPDHYTID--SMHTSDECLYCSPVCKELQYKQECN 77
DB 39 CRECQPHGKVNRCBHTRDLCHPCETGTFYNEAVNDTCQCTQCNH--RSGSELKQNC 96
78 RTHNRVCECKEGRYLIEIFCLKHSRCPGPGVYQAGTPERNTVCKRCPDGFSENETSKA 137
DB 97 PTDVTCRCR-----PGTPRQDSGYKLGVDVCVCPGCHFS--PGNNQ 137
QY 138 PCCKHNCVFGILLTQKNATHDNICSGNS-----EST----- 171
DB 138 ACKPMTNCTLSGKOTRHPASDSIDAVCEDRSLATILMETQRPRTTVQSTVMPRTS 197
QY 172 -----OKVDTHNCPCPAPPELLGSPVFLFPKPKDTLMSRPEVTCVAVY 220
DB 198 ELPSTTLVEPRKCDTHCPCPAPBAGAPSVFLFPKPKDTLMSRPEVTCVAVY 257
QY 221 SHEDPEVKEVMYDGEVHNAAKTPREEOYNSTYRVSVLTVLHODMLNGKEYCKKVSNK 280
DB 258 SHEDPEVKEVMYDGEVHNAAKTPREEOYNSTYRVSVLTVLHODMLNGKEYCKKVSNK 317
QY 281 ALPAPIEKTISAKKGPPEPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGQ 340
DB 318 ALPAPIEKTISAKKGPPEPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGQ 377
QY 341 PENNYKTPPVLDSDGSFFLYSKLTVDKSRMOOGNVSFCSVMHEALHNHYTOKSLSPG 400
DB 378 PENNYKTPPVLDSDGSFFLYSKLTVDKSRMOOGNVSFCSVMHEALHNHYTOKSLSPG 437

RESULT 5

US-08-484-438-10
Sequence 10, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031

GENERAL INFORMATION:

APPLICANT: Piousman, Gregory D.
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegal, Clay B.
APPLICANT: Helistr m, Ingegard
APPLICANT: Helistr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.

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      ZIP: 10036-2711
      COMPUTER READABLE FORM:
      MEDIUM TYPE: Floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Patent Release #1.0, Version #1.25
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/484,438
      FILING DATE: 07-JUN-1995
      CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/323,442
      FILING DATE: 14-OCT-1994
      APPLICATION NUMBER: US 08/150,704
      FILING DATE: 10-NOV-1993
      CLASSIFICATION: 530
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: US 07/981,165
      FILING DATE: 24-NOV-1992
      CLASSIFICATION: 530
      ATTORNEY/AGENT INFORMATION:
      NAME: Mistrock, S. Leslie
      REGISTRATION NUMBER: 18,872
      REFERENCE/DOCKET NUMBER: 5624-230
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: (212) 790-9090
      TELEFAX: (212) 869-8864/9741
      TELEX: 66141 PENNIE
      INFORMATION FOR SEQ ID NO: 10:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 911 amino acids
      TYPE: amino acid
      STRANDEDNESS: unknown
      TOPOLOGY: unknown
      MOLECULE TYPE: protein
      US-08-484-438-10

Query Match      56.5%; Score 1266.5; DB 2; Length 911;
Best Local Similarity 59.6%; Pred. No. 9e-98;
Matches 267; Conservative 23; Mismatches 49; Indels 109; Gaps 16;

      31 QACTAKMTVCAPCPDHYTDS--WHTS-DECLYC-----SPVCKELQYKQECNRTHNR 82
      494 ENCFAE-GMVC-----NHLCSGSGMGSGPDDGLCSGRFSRRICIE----- 534
      83 VCECKEGRYIEF---PCLAKRSCPPGFGVQAGT-----PERNTVC-----K 122
      535 SCNLYDEFFREFENGSLCIE---CDPOCEKMEKEDILTCGPGPNCTKCSHFKDGPNQVC 591
      123 RCPDGF-----FSNETSKAPCRKHTNCSVFGLLNQ--KGNATHDNI---CGSNS 168
      592 KCPDGLGANSFIRKYPADPRECHPC--HPNC-----TGGCNGPPTSHDCTIYPWTGHS 642
      169 -----ESTOKVDRKTHCCPCPAPBELLGSP 192
      643 TLDPDPVKVKALEGFPRLVGPDFGCAEPANTFLDPEPKSCDKTHCCPAPBELLGSP 702
      193 SVFLPFPKPKDLMISRTPEVTCVVDVSHDDPEVKKNWYDGVENAKTKPREBOYNS 252
      703 SVFLPFPKPKDLMISRTPEVTCVVDVSHDDPEVKKNWYDGVENAKTKPREBOYNS 762
      253 TYRVSVALTVLHOMLNCKEYKCVSNKALPAPTEKTSKAKGPREBOYVTLPPSRDEL 312
      763 TYRVSVALTVLHOMLNCKEYKCVSNKALPAPTEKTSKAKGPREBOYVTLPPSRDEL 822
      313 TKNOVSLTCLVKGFPSPDIAEWESNGOPENNKTTPVLDSDGSFFLYSKLTYDKSFMQ 372
      823 TKNOVSLTCLVKGFPSPDIAEWESNGOPENNKTTPVLDSDGSFFLYSKLTYDKSFMQ 882
      373 QGNVSCSVMHALHNHYTKSLSLSPG 400
      883 QGNVSCSVMHALHNHYTKSLSLSPG 910

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      RESULT 6
      US-08-957-063-16
      Sequence 16, Application US/08957063
      Patent No. 6025157
      GENERAL INFORMATION:
      APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
      TITLE OF INVENTION: Neurturin Receptor
      NUMBER OF SEQUENCES: 19
      CORRESPONDENCE ADDRESS:
      ADDRESSEE: Genentech, Inc.
      STREET: 1 DNA Way
      CITY: South San Francisco
      STATE: California
      COUNTRY: USA
      ZIP: 94080
      COMPUTER READABLE FORM:
      MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
      COMPUTER: IBM PC compatible
      OPERATING SYSTEM: PC-DOS/MS-DOS
      SOFTWARE: Mapatin (Genentech)
      CURRENT APPLICATION DATA:
      APPLICATION NUMBER: US/08/957,063
      FILING DATE: 24-Oct-1997
      CLASSIFICATION: 800
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 08/871
      FILING DATE: 9-Jun-1997
      PRIOR APPLICATION DATA:
      APPLICATION NUMBER: 913
      FILING DATE: 18-Feb-1997
      REFERENCE/DOCKET NUMBER: P1086P2
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650/952-9881
      TELEFAX: 650/952-9881
      NAME: Torchia, PhD., Timothy E.
      REGISTRATION NUMBER: 36,700
      REFERENCE/DOCKET NUMBER: P1086P2
      TELECOMMUNICATION INFORMATION:
      TELEPHONE: 650/952-9881
      INFORMATION FOR SEQ ID NO: 16:
      SEQUENCE CHARACTERISTICS:
      LENGTH: 664 amino acids
      TYPE: Amino Acid
      TOPOLOGY: Linear
      US-08-957-063-16

Query Match      55.8%; Score 1249.5; DB 3; Length 664;
Best Local Similarity 63.6%; Pred. No. 1.6e-96;
Matches 264; Conservative 23; Mismatches 57; Indels 71; Gaps 14;

      32 HCRAKMTVCAPCP-DHY-----YTDSWHTSDECLYCSPVCKELQY 72
      274 NCRASYTVTS--CPADYQACLSYAGMIGFDMTPNIVDSPTG---IVVSPMC----- 323
      73 KOECNRTHNRVCECKEGRYIEF---CLKH-----RSCP--PGFVVOAGTP 115
      324 --SCRGSGNMEECF--KFLR-DFTENPCLRNALQAFNGTQDVNVSKGSPFATQAPRV 378
      116 ERNTVCRCPDGFSSNETSKAPCRKHTNCSVFGLLTQKGNATHD-----NICS 165
      379 EKT---PSLPDDLSDSTSLGTSVITCTSVQEOGL-----KANNSKELSMCFELTNIIP 431
      166 GNSESTOKVKTHTCCPCPAPBELLGSPSVLFPKPKDITMISRTPEVTCVVDVSHEDP 225
      432 GPRD---F-DKTHCCPCPAPBELLGSPSVLFPKPKDITMISRTPEVTCVVDVSHEDP 488
      226 EVKFNMTVDQVEVHNATKREGCYNSTYRVSVLTVLHODMTLNGEKYKCVSNKALPAP 285
      489 EVKFNMTVDQVEVHNATKREGCYNSTYRVSVLTVLHODMTLNGEKYKCVSNKALPAP 548
      286 IEKTSKAKGPREBOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAEWESNGOPENN 345

```

Db 549 IEKTSKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIWEMESNGQPENNY 608
QY 346 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNHYTOKSLSLSPG 400
Db 609 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNHYTOKSLSLSPG 663

RESULT 7

US-08-957-063-18
Sequence 18, Application US/08957063
Patent No. 6025157
GENERAL INFORMATION:
APPLICANT: Robert D. Klein, Arnon Rosenthal, Mary A. Hynes
TITLE OF INVENTION: Neurturin Receptor
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/957,063
FILING DATE: 24-Oct-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/871
FILING DATE: 9-Jun-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 913
FILING DATE: 18-Feb-1997
ATTORNEY/AGENT INFORMATION:
NAME: Torchia, Ph.D., Timothy E.
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: P1086P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-8674
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 664 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
08-957-063-18

Query Match 55.7%; Score 1248.5; DB 3: Length 664;
Best Local Similarity 62.7%; Pred. No. 1.9e-96;
Matches 261; Conservative 21; Mismatches 61; Indels 73; Gaps 11;

QY 32 HCTAKMTVACP-DMH-----YTDSWHTSDECLYCSPVCKELQYV 72
Db 274 NCRASRYRTIS-CPADNYOACLSYAGMIGFDMTPNYVDSNPTG---IVVSPMC----- 323
QY 73 KOECNRTNHRVCECKE-----GRVLEIEFCLKHSRCPGFVQAGT 114
Db 324 --NCRSGNNEEBCLEKLRDFTENPCLRNIAQAFNGTDMVMSKPSLP---ATQAPR 377
QY 115 PERNTVCKRCDFGFFSNSTSKAPCRKHTNCSVFGLLTQKGNATHD-----NIC 164
Db 378 VEKT---PSLPDLSSTSTGTSITTCSTIQEGL-----KANSKELSMGFTLTINIS 430
QY 165 SGNESSTOKVDKTCPCPCAPPELLGSPVLFPPKPKDTLMISRTPEVTCVYVDVSHED 224
Db 431 PG---SDPVPDHTCPCPCAPPELLGSPVLFPPKPKDTLMISRTPEVTCVYVDVSHED 487
QY 225 PEVFNMYVDGVEVHNKATKPREQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPA 284

Db 488 PEVFNMYVDGVEVHNKATKPREQYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPA 547
QY 285 PIEKTSKAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGQPENN 344
Db 548 PIEKTSKAGQPREPOVYTLPPSRREMTKNQVSLTCLVKGFPSPDIWEMESNGQPENN 607
QY 345 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNHYTOKSLSLSPG 400
Db 608 KTTTPVLDSDGSFFLYSKLTVDKSRMOQGNVSCSYMHGALHNHYTOKSLSLSPG 663

RESULT 8

US-08-897-236-23
Sequence 23, Application US/08897236A
Patent No. 6075007
GENERAL INFORMATION:
APPLICANT: Regeneron Pharmaceuticals, Inc.
TITLE OF INVENTION: Modified Dorsal Tissue Affecting Factor and Composition
FILE REFERENCE: REG 133
CURRENT APPLICATION NUMBER: US/08/897,236A
CURRENT FILING DATE: 1997-07-17
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 23
LENGTH: 449
TYPE: PRT
ORGANISM: human
US-08-897-236-23

Query Match 55.5%; Score 1243.5; DB 3: Length 449;
Best Local Similarity 73.7%; Pred. No. 2.9e-96;
Matches 244; Conservative 9; Mismatches 17; Indels 61; Gaps 7;

QY 90 RYLEIEFCLHRSQCPGFGVAGTPEPNTVCK-----RCPDGF 129
Db 159 RYVAVGSCFSKRSK-----SVPE-GAVCKPSKSVHLTVLRMRQKRGQRC--GWI 206
QY 130 SNETSKAPCRKHTNCSVFGLLTQKGNATHDNCSSSESTOKVDKTHCPCPABELL 189
Db 207 PIGPIIASEK-----CSG-----DKTHICPCPABELL 237
QY 190 GGSVFLFPPKPKDTLMISTPEVTCVYVDVSHEDPEVKKNMYVDGVEVHNKATKPREQ 249
Db 238 GGSVFLFPPKPKDTLMISTPEVTCVYVDVSHEDPEVKKNMYVDGVEVHNKATKPREQ 297
QY 250 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAGQPREPOVYTLPPSR 309
Db 298 YNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISKAGQPREPOVYTLPPSR 357
QY 310 DELTKNOVSLTCLVKGFPSPDIWEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 369
Db 358 EEMTKNOVSLTCLVKGFPSPDIWEMESNGQPENNYKTTTPVLDSDGSFFLYSKLTVDKS 417
QY 370 RMOQGNVSCSYMHGALHNHYTOKSLSLSPG 400
Db 418 RMOQGNVSCSYMHGALHNHYTOKSLSLSPG 448

RESULT 9
US-08-470-299-4
Sequence 4, Application US/08470299
Patent No. 5783181
GENERAL INFORMATION:
APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkenberg, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21

CORRESPONDENCE ADDRESS:

ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P31005C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090

INFORMATION FOR SEQ ID NO: 4:

SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-470-299-4

Query Match 55.4% Score 1240.5; DB 1; Length 387;

Best Local Similarity 95.8%; Pred. No. 4.3e-96;
Matches 230; Conservative 3; Mismatches 6; Indels 1; Gaps 1;

```
Oy 161 DNICGNSSESTQKVDKTHCPPCPAPELLGSPVFLFPKPKDMLISTREPTCVVVDY 220
    | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 148 DSKCSGTE-PSADKTHCPPCPAPELLGSPVFLFPKPKDMLISTREPTCVVVDY 206
Oy 221 SHEDEVKFNMYVDGVEVHNATKPREEOYNSTYRVSVLVTLVHODWLNKKEYCKKVSNK 280
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 207 SHEDEVKFNMYVDGVEVHNATKPREEOYNSTYRVSVLVTLVHODWLNKKEYCKKVSNK 266
Oy 281 ALPAIEKTISSAKGPRPOVYTLPPSRDELTKNOVSLTCLVKGYPDIWEMESNQ 340
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 267 ALPAIEKTISSAKGPRPOVYTLPPSRDELTKNOVSLTCLVKGYPDIWEMESNQ 326
Oy 341 PENNYKTPPVLDSDGSEFLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 327 PENNYKTPPVLDSDGSEFLYSKLTVDKSRMOQGNVFCSVNHEALHNHYTKSLSPG 386
```

RESULT 10
PCT-US96-10043-9
Sequence 9, Application PC/TUS9610043

GENERAL INFORMATION:

APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA

COUNTRY: USA
ZIP: 02210-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US96/10043

FILING DATE:

CLASSIFICATION:

PRIOR APPLICATION NUMBER: 60/000,213

APPLICATION NUMBER: US 60/000,213

FILING DATE: 14-JUN-1995

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: Lech, Karen F.

REGISTRATION NUMBER:

REFERENCE/DOCKET NUMBER: 00786/284001

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617/542-5070

TELEFAX: 617/542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 442 amino acids

TYPE: amino acid

STRANDEDNESS: not relevant

TOPOLOGY: linear

MOLECULE TYPE: protein

PCT-US96-10043-9

Query Match 55.3% Score 1238.5; DB 4; Length 442;

Best Local Similarity 89.0%; Pred. No. 7.5e-96;
Matches 235; Conservative 6; Mismatches 14; Indels 9; Gaps 2;

```
Oy 142 HTNCSEFGLLTOKGNATHDNCISGNSSTQKV-----DKTHCPPCPAPELLGSPVFL 196
    | | | | | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 182 HT----FPAVLQSSGLVSLSSVTVTPSSDKKVEPKSDKNTHTCPPCPAPELLGSPVFL 237
Oy 197 FPKPKDMLISTREPTCVVVDVSHDEPKFNMYVDGVEVHNATKPREEOYNSTYRV 256
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 238 FPKPKDMLISTREPTCVVVDVSHDEPKFNMYVDGVEVHNATKPREEOYNSTYRV 297
Oy 257 VSVTLVHODWLNKKEYCKKSNKALPAIEKTISSAKGPRPOVYTLPPSRDELTKNO 316
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 298 VSVTLVHODWLNKKEYCKKSNKALPAIEKTISSAKGPRPOVYTLPPSRDELTKNO 357
Oy 317 VSLTCLVKGYPDIWEMESNQGPENNYKTPPVLDSDGSEFLYSKLTVDKSRMOQGNV 376
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 358 VSLTCLVKGYPDIWEMESNQGPENNYKTPPVLDSDGSEFLYSKLTVDKSRMOQGNV 417
Oy 377 FSCSVNHEALHNHYTKSLSPG 400
    | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 418 FSCSVNHEALHNHYTKSLSPG 441
```

RESULT 11
US-08-784-512-3
Sequence 3, Application US/08784512

Patent No. 5872209

GENERAL INFORMATION:

APPLICANT: BARTNIK, Eckart
APPLICANT: EIDENMUELLER, Bernd
APPLICANT: BUTTNER, Frank
APPLICANT: CATERSON, Bruce
APPLICANT: HUGHES, Clare
TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: Suite 500, 3000 K Street, N.W.
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/940,861
FILING DATE: 21-OCT-1992
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15C1P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-940-861-43

```

```

Query Match          55.28; Score 1237; DB 1; Length 347;
Best local Similarity 89.78; Pred. No. 7.3e-96;
Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TOKNATHDNCISG-----NSESTOK----VDKTHTCPCPAPELLGGSVFLEFP 198
      | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : |
Db 85 TVSSSLTLYNTSSDEDEBEYEMESPNIIDTMKFFLYVDKTHCPCPAPELLGGSVFLEFP 144

QY 199 PKPKDTLMISTPEPTVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEDYNSTRYVS 258
      |||||
Db 145 PKPKDTLMISTPEPTVCVVVDVSHEDPEVKFNMYVDGVEVHNATKPREEDYNSTRYVS 204

QY 259 VLTVLHDDMWNGREYKKKYSKALPAPIEKTISKAKGPREPOYYTLPPRSDELTKNOVS 318
      |||||
Db 205 VLTVLHDDMWNGREYKKKYSKALPAPIEKTISKAKGPREPOYYTLPPRSDELTKNOVS 264

QY 319 LTLGVKGFPSPDIAVEWESNGQPENNYKTPRPVLDSGSEFELYSKLTVYKSRMOGNYFS 378
      |||||
Db 265 LTLGVKGFPSPDIAVEWESNGQPENNYKTPRPVLDSGSEFELYSKLTVYKSRMOGNYFS 324

QY 379 CSVMHEALHNHYTQKSLSLSPG 400
      |||||
Db 325 CSVMHEALHNHYTQKSLSLSPG 346

RESULT 13
US-08-459-512-43
; Sequence 43; Application US/08459512
; Patent No. 5728677
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York

```

STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-512-43

Query Match 55.2%; Score 1237; DB 1; Length 347;
Best Local Similarity 89.7%; Pred. No. 7.3e-96;

Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQKGNATHDNICSG-----NSESTQK---VDKTHTCPCPAPAPELLGSPVFLFP 198
DB 85 TVSGSLITINLTSDEDEYEMESPNTIDMKFFLYVDKTHTCPCPAPAPELLGSPVFLFP 144
QY 199 PKPKDTLMISRPEVTCVAVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVVS 258
145 PKPKDTLMISRPEVTCVAVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVVS 204
QY 259 VLTIVHOMLNKEKCKVSKNAPAPIEKTSKAKGPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTIVHOMLNKEKCKVSKNAPAPIEKTSKAKGPREPOVYTLPPSRDELTKNOVS 264
QY 319 LTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOQGNVS 378
DB 265 LTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOQGNVS 324
QY 379 CSVMHEALHNHTOKSLSPG 400
DB 325 CSVMHEALHNHTOKSLSPG 346

RESULT 14
US-08-459-657-43
Sequence 43, Application US/08459657
Patent No. 5914111
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
FUNCTION ASSOCIATED ANTIGEN 3

NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,657
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-657-43

Query Match 55.2%; Score 1237; DB 2; Length 347;
Best Local Similarity 89.7%; Pred. No. 7.3e-96;

Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQKGNATHDNICSG-----NSESTQK---VDKTHTCPCPAPAPELLGSPVFLFP 198
DB 85 TVSGSLITINLTSDEDEYEMESPNTIDMKFFLYVDKTHTCPCPAPAPELLGSPVFLFP 144
QY 199 PKPKDTLMISRPEVTCVAVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVVS 258
DB 145 PKPKDTLMISRPEVTCVAVDVSHEDPEVKFNWYDGVGVHNAKTKPREEOYNSTYRVVS 204
QY 259 VLTIVHOMLNKEKCKVSKNAPAPIEKTSKAKGPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTIVHOMLNKEKCKVSKNAPAPIEKTSKAKGPREPOVYTLPPSRDELTKNOVS 264
QY 319 LTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOQGNVS 378
DB 265 LTCLVKGFPSPDIAVWESNGOPENNYKTPPVLDSDGSFFLYSKLTVDKSRMOQGNVS 324
QY 379 CSVMHEALHNHTOKSLSPG 400
DB 325 CSVMHEALHNHTOKSLSPG 346

RESULT 15
US-08-460-132-43
Sequence 43, Application US/08460132
Patent No. 5928643
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.

APPLICANT: WALINER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,132
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991

ATTORNEY/AGENT INFORMATION:

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INFORMATION FOR SEQ ID NO: 43:

SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-132-43

Query Match

Best Local Similarity 55.2%; Score 1237; DB 2; Length 347;
Matches 235; Conservative 2; Mismatches 11; Indels 14; Gaps 2;

QY 153 TQGNATHNIGSG-----NSESTOK---VDKTHTCPPAPELGSPVFLFP 198
DB 85 TVSGSLITNLTSDEDEYEMESPNTDTMKFLLYDKTHTCPPAPELGSPVFLFP 144
QY 199 PKPKDTLMSRPEVTCVVVDSHEDPEVFNMYVDGVEVHNAKTRPREOYNSTRVVS 258
DB 145 PKPKDTLMSRPEVTCVVVDSHEDPEVFNMYVDGVEVHNAKTRPREOYNSTRVVS 204
QY 259 VLTVLHQMNLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVYTLPPSRDELTKNOVS 318
DB 205 VLTVLHQMNLNGKEYCKVSNKALPAPIEKTIKAKGQPREPOVYTLPPSRDELTKNOVS 264
QY 319 LTCLVKGFPSPDIAVEMESGQPENNYKTPPYLSDSGSFELYSKLTVDKSRMOQGNVFS 378
DB 265 LTCLVKGFPSPDIAVEMESGQPENNYKTPPYLSDSGSFELYSKLTVDKSRMOQGNVFS 324
QY 379 CSVMHEALHNHYTQKSLSPG 400
DB 325 CSVMHEALHNHYTQKSLSPG 346

Search completed: December 27, 2000, 10:53:56
Job time: 147 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:54:37 ; Search time 40.66 Seconds
(without alignments)
624.301 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240
Sequence: 1 ETPEPKYLHDETSKSLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 182106 seqs, 63460219 residues

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : PIR_65:*

1: PIR1: *
2: PIR2: *
3: PIR3: *
4: PIR4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1234	55.1	330	1	IGHU
2	1230	54.9	374	2	Ig gamma-1 chain C
3	1229	54.9	255	4	Ig heavy chain V r
4	1225	54.7	374	2	Ig gamma-1 chain C
5	1183.5	52.8	234	2	Ig heavy chain V r
6	1154.5	51.5	377	2	Ig gamma-3 chain C
7	1152.5	51.5	377	2	Ig gamma-3 chain C
8	1148.5	51.3	326	1	Ig gamma-2 chain C
9	1136	50.7	327	1	Ig gamma-4 chain C
10	1133.5	50.6	289	1	Ig gamma-3 heavy C
11	923	41.2	323	1	Ig gamma chain C r
12	917.5	41.0	328	2	Ig gamma 2b chain
13	917.5	41.0	328	2	Ig gamma 2a chain
14	915.5	40.9	277	2	Ig gamma 4 chain C
15	904.5	40.4	329	1	Ig gamma-2 chain C
16	895.5	40.0	328	2	Ig gamma-1 chain C
17	889.5	39.7	328	2	Ig gamma 3 chain C
18	861.5	38.5	470	2	Ig heavy chain pre
19	851.5	38.0	308	2	Ig heavy chain C r
20	847.5	37.8	329	1	Ig gamma-1 chain C
21	847.5	37.8	329	1	Ig gamma-3 chain C
22	843	37.6	333	2	Ig gamma-2b chain
23	841.5	37.6	398	1	Ig gamma-3 chain C
24	830	37.1	444	1	Ig gamma-1 chain C
25	820	36.6	324	1	Ig gamma-1 chain C
26	820	36.6	326	2	Ig gamma-1 chain C
27	820	36.6	330	1	Ig gamma-1 chain C
28	812.5	36.3	330	1	Ig gamma-2a chain
29	812.5	36.3	399	1	Ig gamma-2a chain

30	812.5	36.3	469	2	Ig gamma-2a chain
31	804.5	35.9	329	2	Ig gamma-2c chain
32	802.5	35.8	446	2	Ig gamma-2a chain
33	801.5	35.8	335	1	Ig gamma-2a chain
34	791	35.3	322	2	Ig gamma-2a chain
35	777.5	34.7	336	1	Ig gamma-2b chain
36	777.5	34.7	405	1	Ig gamma-2b chain
37	777.5	34.7	474	2	Ig gamma-2b chain
38	766	34.2	327	2	Ig gamma-2b chain
39	755.5	33.7	475	2	Ig gamma-2b chain
40	702	31.3	180	2	Ig gamma heavy chain
41	574.5	25.6	218	2	Ig heavy chain V-I
42	572.5	25.6	249	2	Ig heavy chain VHI
43	566	25.3	152	2	Ig gamma-1 chain C
44	397.5	17.7	572	2	Ig heavy chain (
45	374	16.7	549	2	Ig heavy chain pre

ALIGNMENTS

RESULT 1

IGHU
Ig gamma-1 chain C region - human
C:Species: Homo sapiens (man)
C:Date: 31-Jan-1981 #sequence-revision 18-Aug-1982 #text-change 16-Jul-1999
C:Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91223; A02146
R:Ellison, J.W.; Berson, B.J.; Hood, L.E.
Nucleic Acids Res. 10, 4071-4079, 1982
A:Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.
A:Reference number: A93433; MUID:82274238
A:Accession: A93433
A:Molecule type: DNA
A:Residues: 1-330 <ELD>
A:Cross-references: EMBL:217370
A:Note: this sequence has the Gln(17) allelotypic marker, 97-Lys, and the Gln(1) marker
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:217370
R:Yakushiji, N.; Ueda, S.; Ohta, M.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113:235-330 <TAK>
A:Cross-references: EMBL:217370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gamma6-immunoglobulin. VII. Amino acid seq
A:Reference number: A90563; MUID:71064024
A:Accession: B90563
A:Contents: myeloma protein Eu
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-135 <GUN>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gamma6-immunoglobulin. VIII. Amino acid se
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: protein
A:Residues: 136-154, 'Q', '156-165, 'Q', '167-176, 'Q', '178-194, 'N', '196-197, 'D', '199-238, 'E', '2
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponting, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primärstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein N1

igen Primerstruktur.
A:Reference number: A91668; MUID:77070269.
A:Contents: myeloma protein Nie
A:Accession: B91668
A:Molecule type: protein
A:Residues: 1-34, 'Q', '36-96', 'K', '98-115', 'Q', '117-197', 'D', '199-238', 'D', '240', 'L', '242-268', 'E', '27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des Kristallisationsreagen monoklonalen Immunglobulins IgG1 KOL
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOL; disulfide bonds
A:Accession: A91723
A:Molecule type: protein
A:Residues: 1-96, 'R', '98-197', 'D', '199-238', 'E', '240', 'W', '242-266', 'D', '268-271', 'D', '273-330' <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Call, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Drexler, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
embionide cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMIM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 114/1, 224/1
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a
C:Superfamily: Immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:137-306/Domain: immunoglobulin homology <IM1>
F:243-310/Domain: immunoglobulin homology <IM3>
F:27-83,144-204,250-308/Disulfide bonds: #status experimental
F:103/Disulfide bonds: interchain (to light chain) #status experimental
F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental
F:180/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 55.1%; Score 1234; DB 1; Length 330;
Best Local Similarity 92.1%; Pred. No. 1.2e-68;
Matches 22; Conservative 4; Mismatches 6; Indels 10; Gaps 2;

QY 159 THDNICS-----GNSESTOKY-----DKTHCPCPCPAPPELLGGPSVFLFPPPKDTLMIS 208
DB 78 TQYTCVNVNHPKSTKDKKVEPSCDTHCPCPCPAPPELLGGPSVFLFPPPKDTLMIS 137
QY 209 RTEVETCVVDVSHEDPEVFNMYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMWL 268
DB 138 RTEVETCVVDVSHEDPEVFNMYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMWL 197
QY 269 NGKEYKCKVSKKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFY 328
DB 198 NGKEYKCKVSKKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFY 257
QY 329 SDIAEVESNGQPPNNKTPPVLDSDGSFELYSKLTVDSKRMQOGNVFCSVNHAEALHN 388
DB 258 SDIAEVESNGQPPNNKTPPVLDSDGSFELYSKLTVDSKRMQOGNVFCSVNHAEALHN 317
QY 389 HYTOKSLSLSPG 400
DB 318 HYTOKSLSLSPG 329

RESULT 2
S72664
Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000
C:Accession: S72664
R:Khamlich, A.A.
submitted to the EMBL Data Library, September 1994
A:Reference number: S72664
A:Accession: S72664
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <RNA>
A:Cross-references: EMBL:X81695
C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 54.9%; Score 1230; DB 2; Length 374;
Best Local Similarity 93.1%; Pred. No. 2.5e-68;
Matches 228; Conservative 4; Mismatches 9; Indels 4; Gaps 1;

QY 156 GNATHDNICGNSGNSQKVDKTHCPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTC 215
DB 133 GGGTLVTVC-----EPKSCDKTHCPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTC 188
QY 216 VVDVSHEDPEVFNMYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMLNGKEYKC 275
DB 189 VVDVSHEDPEVFNMYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMLNGKEYKC 248
QY 276 KVSNNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYSDIAVEW 335
DB 249 KVSNNKALPAPIEKTISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYSDIAVEW 308
QY 336 ESNQGPENNNKTPPVLDSDGSFELYSKLTVDSKRMQOGNVFCSVNHAEALHNHYTOKSL 395
DB 309 ESNQGPENNNKTPPVLDSDGSFELYSKLTVDSKRMQOGNVFCSVNHAEALHNHYTOKSL 368
QY 396 SLSPG 400
DB 369 SLSPG 373

RESULT 3
S31866
Ig gamma-1 chain C region - synthetic
C:Species: synthetic
A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli
C:Date: 06-Jan-1995 #sequence_revision 17-Mar-1997 #text_change 19-May-2000
C:Accession: S31866
A:Description: Screening method for protein-protein interactions of cloned gene produc
submitted to the EMBL Data Library, February 1993
A:Reference number: S31866
A:Accession: S31866
A:Molecule type: mRNA
A:Residues: 1-255 <FLV>
A:Cross-references: EMBL:X70421; NID:g33068; PIDN:CAA49866.1; PID:g33069
C:Keywords: immunoglobulin
F:1-22/Region: Escherichia coli outer membrane protein A precursor
F:23-25/Region: human Ig gamma-1 chain C region

Query Match 54.9%; Score 1229; DB 4; Length 255;
Best Local Similarity 98.3%; Pred. No. 1.9e-68;
Matches 226; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 171 TQYVDKTHCPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKN 230
DB 25 SKSCDKTHCPCPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKN 84
QY 231 WYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMLNGKEYKCKVSKKALPAPIEKT 290
DB 85 WYVDGEVHNATKPREEOYNSTYRVSVLTVDHOMLNGKEYKCKVSKKALPAPIEKT 144
QY 291 SKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAEVESNGQPPNNKTPP 350

Db 145 SKAAGPREOYVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGOPENNYKTTP 204

QY 351 VLDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 400

Db 205 VLDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 254

RESULT 4

S69339

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C>Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 17-Mar-2000

C:Accession: S69339

R:Khamlich, A.A.; Anconturier, P.; Preud'homme, J.L.; Cogne, M.

Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.

A:Reference number: S69339; MUID:95262687

A:Accession: S69339

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

C:Cross-references: EMBL:X81695

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match 54.7%; Score 1225; DB 2; Length 374;

Best Local Similarity 96.6%; Pred. No. 5e-68;

Matches 225; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 168 SESTQKVDKHTCPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEV 227

Db 141 SSEPKSCDKHTCPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEV 200

QY 228 KFNWYDGVFNHNAKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNKALPAPIE 287

Db 201 KFNWYDGVFNHNAKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNKALPAPIE 260

QY 288 KITSKAGPREOYVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGOPENNYKT 347

Db 261 KITSKAGPREOYVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGOPENNYKT 320

QY 348 TPPLVDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 400

Db 321 TPPLVDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 373

RESULT 5

PT0207

Ig gamma chain C region - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C>Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999

C:Accession: PT0207

R: Ehrlich, P.H.; Moustafa, Z.A.; Oestberg, L.

Mol. Immunol. 28, 319-322, 1991

A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.

A:Reference number: PT0207; MUID:91287716

A:Accession: PT0207

A:Molecule type: mRNA

A:Residues: 1-234 <EHR>

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:48-117/Domain: immunoglobulin homology <IMM>

Query Match 52.8%; Score 1183.5; DB 2; Length 234;

Best Local Similarity 94.4%; Pred. No. 1.1e-65;

Matches 221; Conservative 1; Mismatches 3; Indels 9; Gaps 1;

QY 170 STOKVNDK-----THTCPPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDV 220

Db 1 SNTRKVDKPKSCDTHTCPPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDV 60

QY 221 SHEDPEVKFNWYDGVFNHNAKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNK 280

Db 61 SHEDPEVKFNWYDGVFNHNAKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNK 120

QY 261 ALPAPIEKTISKAKGPREOYVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGQ 340

Db 121 ALPAPIEKTISKAKGPREOYVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGQ 180

QY 341 PENNYKTTPVLDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKS 394

Db 181 PENNYKTTPVLDSGSEFLYKSLTVDSKRWQGNVSCSYMEHALHNHYTQKS 234

RESULT 6

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C>Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human immunoglobulin gamma 3 heavy chain constant region gene.

A:Reference number: A23511; MUID:86148507

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: GB:X03604; GB:M2958; NID:933070; PIDN:CAA27268.1; PID:9577056

C:Genetics:

A:Gene: IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Insertions: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Query Match 51.5%; Score 1154.5; DB 2; Length 377;

Best Local Similarity 67.1%; Pred. No. 1e-63;

Matches 228; Conservative 19; Mismatches 32; Indels 61; Gaps 7;

QY 76 CNRTNHRVCEKRGYLEIEF-----CLKHSK---PPGCVVAGTPEPNTVC 121

Db 83 CNVNH-KPSNTKVDKRELKTPGDTTHTCPPCEPSCPTPP-----C 126

QY 122 KCPDGFSSNETSKAP-CKHTNCSVFGLLTQKNATHDNIGSSESTQKVDKTHTC 180

Db 127 PCPEP-KSCDTPPCPCPEPSC-----DTPPC 156

QY 181 PCPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVFN 240

Db 157 PCPAPPELLGSPVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVFN 216

QY 241 AKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNKALPAPIEKTISKAKGPREP 300

Db 217 AKTRPREQYNSTYRVVSVLTVLDHQMINKKEYCKVSNKALPAPIEKTISKAKGPREP 276

QY 301 QVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGOPENNYKTTPVLDSGSEFL 360

Db 277 QVTLPPSRDELTKNOVSLCTVKGFFPSDIAVWESNGOPENNYKTTPVLDSGSEFL 336

QY 361 YSKLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 400

Db 337 YSKLTVDSKRWQGNVSCSYMEHALHNHYTQKSLSPG 376

RESULT 7

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C>Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A: Molecule type: protein
A: Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 194-200
A: Note: this sequence has since been revised

DNA 1, 11-18, 1981
 A:Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene
 A:Reference: A90933, MID:83157104
 A:Accession: A90933

A: Molecule type: protein
A: Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 194-200
A: Note: this sequence has since been revised

```

A:Residues: 12-97 <MIC>
A>Note: the hinge region in gamma-3 chains is about four times as long as in other ga
idue segment (12-28)
A>Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form an
R:Moldenstein,Todcl,C.; Frangione,B.; Prelli,F.; Franklin,E.C.
Biochem.Biophys.Res.Commun.71,907-914,1976
A>Title: The amino acid sequence of "heavy chain disease" protein ZUC. Structure of t
A:Reference number: A90198; MUID:77021516
A:Contents: heavy chain disease protein Zuc, partial sequence corresponding to residu
A:Accession: A90198
A:Molecule type: protein
A:Residues: 59-125,'BB','128-226,228-289 <MO>
A>Note: this protein lacks most of the V region, all of the CH1 region, and part of t
R:Alexander,A.; Steinmetz,M.; Barillaull,D.; Frangione,B.; Franklin,E.C.; Hood,
Proc.Natl.Acad.Sci.U.S.A.79,3260-3264,1982
A>Title: gamma heavy chain disease in man: cDNA reference supports partial gene deleti
A:Reference number: A93915; MUID:82247835
A:Contents: heavy chain disease protein Omn
A:Accession: A93915
A:Molecule type: mRNA
A:Residues: 12-70;72-114,116-135,'E','127-133','L','135-136','E','138','Y',140-154,'D',156-
A>Note: a carboxyl-terminal Lys is removed posttranslationally
A>Note: this sequence may represent an allelic form or another gamma chain subclass
C:Comment: The heavy chain disease protein Wis is shown.
C:Genetics:
A:Gene: GDB:IGHG3
A:Cross-references: GDB:119339; OMIM:147120
A:Map position: 14q32.33-14q32.33
A:Superfamily: immunoglobulin C region; immunoglobulin homology
C:Keywords: duplication; glycoprotein; immunoglobulin; pyroglutamic acid
F:203-270/Domian: immunoglobulin homology <IMM>
F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F:6,140/Binding site: carbonylurate (Asn) (covalent) #status experimental

Query Match          50.6%   Score 1133.5: DB 1: Length 289:
Best Local Similarity 70.8%   Pred. NO.1.5e-62:
Matches 218: Conservative 19: Mismatches 22: Indels 49: Gaps 5:

Oy      97 CLKHSC---PPGFVWAGTPTERTWCRCPCDPGFSSNETSKAP-CRKHTNCVFGLL 152
       |::|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      27 CEPKSCOTPPP-----CPKCPKP-KSCDTPPCPCPCPCPSC-----+63

Oy      153 TQKNATHDNICSGNSESTOKVDKTHTCPCPCAPELLGGPSVFLFPKPKDTLMISRPPE 212
       ||-----|-----DTPPCPCPCPCAPELLGGPSVFLFPKPKDTLMISRPPE 101
Db      64 -----DTPPCPCPCPCAPELLGGPSVFLFPKPKDTLMISRPPE 101

Oy      213 VTCCVVVDSDHEDEPKFMWYDVGVENAKKKPREEOVNSRYRVSVLTJLVHOMLNKE 272
       |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      102 VTCVVVDSDHEDEPVQEFWMYDVGVENAKKKPRQGNSTFRVAVSLTVJLVHOMLDKE 161

Oy      273 YCKKSNKLPAPIEKITSKAKGPCREPOVTLPPSRDELTKNOVSILCLVKGEFYPSDIA 332
       |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      162 YCKKSNKLPAPIEKITSKKGGRPREQVYTLTPRSREMKNNQVSLCLVKGYPSDIA 221

Oy      333 VEWHSNGOPENNKTTPPYVLDSGSFFLYSKLYDKSMQOGNVFSQVMHEALHNHYTO 392
       |||||||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db      222 VEWESSGQPENNNTTPPMLDSDGSFFLYSKLYDKSRMQGNIFSCVMHEALHNRFYO 281

Oy      393 KSLSLSPG 400
       |||||||
Db      282 KSLSLSPG 289

RESULT 11
GHRB
Ig gamma chain C region - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 24-Apr-1994 #sequence.revision 15-Nov-1984 #text.change 16-Jul-1999
C:Accession: A91749; A90290; A93928; A90245; A94416; A02161
R:Bernstein, R.E.; Alexander, C.B.; Mage, R.G.
Immunogenetics 18, 387-397, 1983
A>Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-1 haplo

```

A:Reference number: A91749; MUID:84030930
 A:Accession: A91749
 A:Molecule type: mRNA
 A:Residues: 1-323 <BERR>
 A:Note: This sequence has the d12 allotypic marker, 104-Thr, and the e14 marker, 185-Thr
 R:Pratt, D.M.; Mole, L.E.
 Biochem. J. 151, 337-349, 1975
 A:Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglobulin
 A:Reference number: A90290; MUID:76135469
 A:Accession: A90290
 A:Molecule type: protein
 A:Residues: 1-47, 'E', '49-71', 'PV', '72-128' <PRA>
 R:Matsumoto, C.L.; Moore, K.W.; Steimetz, M.; Hood, L.; Knight, K.L.
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982
 A:Title: Heavy chain genes of rabbit IgG: isolation of a cDNA encoding gamma heavy chain
 A:Reference number: A93928; MUID:83299917
 A:Accession: A93928
 A:Molecule type: mRNA
 A:Residues: 88-103, 'M', '105-143', 'E', '145-184', 'A', '186', 'E', '188-266' <MAR>
 A:Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic marker
 R:Frutiger, J.E.; Jackson, S.A.; Mole, L.E.; Porter, R.R.
 Biochem. J. 116, 249-259, 1970
 A:Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin
 A:Reference number: A90245; MUID:70110015
 A:Accession: A90245
 A:Molecule type: protein
 A:Residues: 132-143, 'E', '145-161' <FRU>
 R:Hall, R.L.; Lebovitz, H.E.; Fellows Jr., R.E.; Delaney, R.
 In Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp. 109-127, Almqvist and Wiksell, A:Reference number: A94416
 A:Accession: A94416
 A:Molecule type: protein
 A:Residues: 129-131, '155-172', 'D', '174-184', 'A', '186', 'E', '188-200', 'D', '202-217', 'E', '219-232', 'Q', 'A:Note: this has the e15 allotypic marker. 185-Ala
 C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa) chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16 C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
 F:20-82/Domain: immunoglobulin homology <IM1>
 F:130-199/Domain: immunoglobulin homology <IM2>
 F:236-303/Domain: immunoglobulin homology <IM3>
 F:173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 41.2%; Score 923; DB 1; Length 323;
 Best Local Similarity 61.5%; Pred. No. 1.2e-49;
 Matches 177; Conservative 33; Mismatches 46; Indels 32; Gaps 5;

123 RCPDGFES-----NETSSKAPCRKHTNCSVGLLLTQKGNATHDNICSGNSESTOKVDT 177
 Db 57 RQSGGLVSLSSVSTSSQ-----VTCNV-----AHATNTKVDKT 94

178 ---HTC--PPCPAPBELLGSPVFLFPPPKDLMISRPEVTCVVDVSHDEPEVKFNW 232
 Db 95 VAPSTCSKPTCPPELLGSPVFLFPPPKDLMISRPEVTCVVDVSHDEPEVKFNW 154

233 VDGEVHNAAKTKPREQVNTYRVSVLTJLVHODMLNGEKVKCKSNKALPAPIETKTS 292
 Db 155 INNEQVRAKRPPLLEQOQNSTIRVSTLPITHDMLRKERCKVHNKALPAPIETKTS 214

293 AKGPREFQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMVESNGOPENNYKTTTPVL 352
 Db 215 ARGPDLERKVTYTMGPRLSRSVSLTCLMNGFPSPDISVEMENKGAEDNYKTTTPVL 274

353 DSDGSFLYSLKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPG 400
 Db 275 DSDGSFLYSLKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPG 322

RESULT 12
 147160
 Ig gamma 2b chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: 147160
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
 A:Reference number: 147158; MUID:95015845
 A:Accession: 147160
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52218.1; PID:9433126
 C:Genetics:
 A:Gene: IgG2b
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM3>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
 Best Local Similarity 60.5%; Pred. No. 2.6e-49;
 Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;

125 PDGFSNETSSKAPC---RKHTNCSVFGLLTQKGNATHDNICSGNSESTOKVDT--T 177
 Db 59 PSGLYSLSMVTVPASSLSKSTTCNV-----NHPATTTKVDKRVGT 100

178 HTCPPCP-----APBELLGSPVFLFPPPKDLMISRPEVTCVVDVSHDEPEVKFNW 231
 Db 101 KTKPCPCPCACESP---GSPVFIFPPPKDLMISRPEVTCVVDVSHDEPEVKFNW 156

232 YVDGEVHNAAKTKPREQVNTYRVSVLTJLVHODMLNGEKVKCKSNKALPAPIETKTS 291
 Db 157 YVDGEVHNAAKTKPREQVNTYRVSVLTJLVHODMLNGEKVKCKSNKALPAPIETKTS 216

292 KAKGPREFQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMVESNGO--PENNYKTTTP 349
 Db 217 KAKGPREFQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMVESNGOPEPEGNKTTTP 276

350 PVLSDGSFLYSLKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPG 400
 Db 277 PVDGVTGYFLYSLKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPG 327

RESULT 13
 147159
 Ig gamma 2a chain constant region - pig (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
 C:Accession: 147159
 R:Kacskovics, I.; Sun, J.; Butler, J.E.
 J. Immunol. 153, 3565-3573, 1994
 A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of
 A:Reference number: 147158; MUID:95015845
 A:Accession: 147159
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-328 <KAC>
 A:Cross-references: EMBL:U03779; NID:9433123; PIDN:AAA52217.1; PID:9433124
 C:Genetics:
 A:Gene: IgG2a
 C:Superfamily: immunoglobulin C region; immunoglobulin homology
 F:133-202/Domain: immunoglobulin homology <IM3>

Query Match 41.0%; Score 917.5; DB 2; Length 328;
 Best Local Similarity 60.5%; Pred. No. 2.6e-49;
 Matches 176; Conservative 35; Mismatches 43; Indels 37; Gaps 6;

125 PDGFSNETSSKAPC---RKHTNCSVFGLLTQKGNATHDNICSGNSESTOKVDT--T 177
 Db 59 PSGLYSLSMVTVPASSLSKSTTCNV-----NHPATTTKVDKRVGT 100

178 HTCPPCP-----APBELLGSPVFLFPPPKDLMISRPEVTCVVDVSHDEPEVKFNW 231


```

Db      101 KTRPPCPICACSP-----GPSVFIRPPKPKDLMISRTQVTCVVDVSDENPEVOFSW 156
      232 YVDGEVHNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTIS 291
      157 YVDGEVHNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTIS 216
      292 KAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTP 349
      217 KAGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTP 276
      350 PVDSDGSEFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTOKSLSPG 400
      277 PQDDVDTYLYSKFVYDKASWOGGIFQCAVHMEALHNHYTOKSLSPG 327

RESULT 14
14162
Ig gamma 4 chain constant region - pig (fragment)
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 21-Feb-1997 #sequence: revision 21-Feb-1997 #text-change 21-Jan-2000
Accession: I47162
R:Kacskovics, I.; Sun, J.; Butler, J.E.
J. Immunol. 153, 3565-3573, 1994
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a
A:Reference number: I47158; MUID:95015845
A:Accession: I47162
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-277 <KAC>
A:Cross-references: EMBL:003782; NID:g433129; PIDN:AAA52220.1; PID:g433130
C:Genetics:
A:Gene: IgG4
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
F:82-151/Domain: Immunoglobulin homology <IMM>

Query Match      40.9%; Score 915.5; DB 2; Length 277;
Best Local Similarity 61.3%; Pred. No. 2.9e-49;
Matches 176; Conservative 34; Mismatches 48; Indels 29; Gaps 6;

      125 PDGFSENETSSKAPC---RKHTNCSVFGLLTQKGNATHNDCSGNSESTOKYDK--T 177
      8  PSLYLSSKWTVPASSLSKSTCNV-----NHPAITTVYDKRGT 49
      178 HTCPPCP-APELLG-GPSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVFNMYVDG 235
      50 KTRPPCPICACSPGPSAFIRPPKPKDLMISRTPEVTCVVDVSDENPEVOFSWYVDG 109
      236 VEYHNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTISKAG 295
      110 VEYHNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTISKAG 169
      296 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTPVD 353
      170 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTPVD 229
      354 SDGSEFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTOKSLSPG 400
      230 VDDTYFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTOKSLSPG 276

RESULT 15
1526P
Ig gamma-2 chain C region - guinea pig
C:Species: Cavia porcellus (guinea pig)
C:Date: 07-May-1981 #sequence: revision 07-May-1981 #text-change 16-Jul-1999
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151
R:Trischmann, T.M.
submitted to the Atlas, April 1975
A:Reference number: A94553
A:Accession: A94553
A:Molecule type: protein

```

```

A:Residues: 1-3 <TR>
R:Birshtein, B.K.; Huseaid, O.Z.; Cebra, J.J.
Biochemistry 10, 18-25, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III.
A:Reference number: A90352; MUID:71058471
A:Accession: A90352
A:Molecule type: protein
A:Residues: 4-68 <BIR>
R:Turner, K.J.; Cebra, J.J.
Biochemistry 10, 9-17, 1971
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II.
A:Reference number: A90359; MUID:71058486
A:Accession: A90359
A:Molecule type: protein
A:Residues: 69-133; 312-329 <TUR>
R:Tracey, D.E.; Cebra, J.J.
Biochemistry 13, 4796-4803, 1974
A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibody
A:Reference number: A90384; MUID:75036072
A:Accession: A90384
A:Molecule type: protein
A:Residues: 134-226 <TRA>
R:Trischmann, T.M.; Cebra, J.J.
Biochemistry 13, 4804-4811, 1974
A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibody
A:Reference number: A90385; MUID:75036073
A:Accession: A90385
A:Molecule type: protein
A:Residues: 227-311 <TR2>
R:Oliveira, B.; Lamu, M.E.
Biochemistry 10, 26-31, 1971
A:Title: Interchain disulfide bridges of guinea pig gamma-2 immunoglobulin.
A:Reference number: A90354; MUID:71058474
A:Contents: annotation; disulfide bonds
A:Note: Cys-16 is involved in a heavy-light chain bond
A:Note: Cys-105, Cys-107, and Cys-110 form inter-heavy chain bonds
C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.
C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C:Superfamily: Immunoglobulin C region; Immunoglobulin homology
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:21-81/Domain: Immunoglobulin homology <IM1>
F:135-204/Domain: Immunoglobulin homology <IM2>
F:241-310/Domain: Immunoglobulin homology <IM3>
F:28-79/Disulfide bonds: #status experimental
F:142-202/Disulfide bonds: #status experimental
F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental
F:248-308/Disulfide bonds: #status experimental

Query Match      40.4%; Score 904.5; DB 1; Length 329;
Best Local Similarity 60.3%; Pred. No. 1.6e-48;
Matches 173; Conservative 30; Mismatches 53; Indels 31; Gaps 3;

      127 GFSENETSSKAPCKRTNCSVFGLLTQKGNATHNDCSGNSESTOKYDKT----- 177
      61 GLYSLTSMVTVPSSQKATCNV-----AHPASSTKVTVEPIRTPP 102
      178 --HTCPPCAPPELLGSPVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVFNMYVDG 235
      103 BPCTCKPCPPENLGGPSAFIRPPKPKDLMISRTPEVTCVVDVSDENPEVOFTFVON 162
      236 VEYHNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTISKAG 295
      163 KPVGNNAKTRPREBOYNSTRVSVLTVLHODWLNKGEYCKCKVSNKALPAPIEKTISKAG 222
      296 QPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTPVD 353
      223 APMPDPVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGO--PENNYKTTTPVD 282
      354 SDGSEFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTOKSLSPG 400
      283 ADGSIYFLYSKLTVDKSRMOGNGVSCSVHMEALHNHYTOKSLSPG 329

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Thu Dec 28 15:09:22 2000

us-09-389-545-5.rpr

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Search completed: December 27, 2000, 10:54:39
Job time: 190 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:55:05 ; Search time 24.16 Seconds

(without alignments)
528.939 Million cell updates/sec

Title: US-09-389-545-5

Sequence: 1 ETPPKYLYHDETSQQLC.....VMHEALHNHYTKSLISLSPG 400

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	55.1	330	1 GCL_HUMAN	P01857 homo sapien
2	1148.5	51.3	326	1 GCL_HUMAN	P01859 homo sapien
3	1136	50.7	327	1 GCL_HUMAN	P01861 homo sapien
4	1133.5	50.6	290	1 GCL_HUMAN	P01860 homo sapien
5	923	41.2	323	1 CC_RABIT	P01870 oryctolagus
6	904.5	40.4	329	1 CC2_CAVO	P01862 cavia porce
7	847.5	37.8	329	1 GCL_MOUSE	P20761 rattus norv
8	843	37.6	333	1 GCB_RAT	P03987 mus musculu
9	841.5	37.6	338	1 GCB_MOUSE	P01868 mus musculu
10	820	36.6	324	1 GCL_MOUSE	P01868 mus musculu
11	820	36.6	326	1 GCL_RAT	P20789 rattus norv
12	820	36.6	335	1 GCL_MOUSE	P01869 mus musculu
13	812.5	36.3	330	1 GCB_MOUSE	P01863 mus musculu
14	812.5	36.3	339	1 GCAM_MOUSE	P01865 mus musculu
15	804.5	35.9	329	1 GCC_RAT	P20762 rattus norv
16	801.5	35.8	335	1 GCB_MOUSE	P01864 mus musculu
17	791	35.3	322	1 GCA_RAT	P20760 rattus norv
18	777.5	34.7	336	1 GCB_MOUSE	P01866 mus musculu
19	777.5	34.7	405	1 GCB_MOUSE	P01867 mus musculu
20	365.5	16.3	391	1 MUCB_HUMAN	P04220 homo sapien
21	361	16.1	421	1 EPC_MOUSE	P06336 mus musculu
22	360	16.1	454	1 MUC_HUMAN	P01871 homo sapien
23	354.5	15.8	455	1 MUC_MOUSE	P01872 mus musculu
24	353	15.8	428	1 EPC_HUMAN	P01874 homo sapien
25	353	15.8	428	1 EPC_MOUSE	P01874 mus musculu
26	349.5	15.6	476	1 MUCB_MOUSE	P01873 mus musculu
27	345.5	15.4	461	1 TNR2_HUMAN	P20333 homo sapien
28	340	15.2	458	1 MUC_RABIT	P03988 oryctolagus
29	340	15.2	474	1 TNR2_MOUSE	P25119 mus musculu
30	338.5	15.1	450	1 MUC_CANFA	P01874 canis famill
31	335	15.0	479	1 MUC_RABIT	P04221 oryctolagus
32	333.5	14.9	454	1 MUC_MESAU	P06337 mesocricetu
33	332.5	14.8	457	1 MUC_SUNMU	P20768 suncus murt

ALIGNMENTS

RESULT	ID	STANDARD	PRT	330 AA.
1	GCL_HUMAN			
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	15-JUL-1999 (Rel. 38, Last annotation update)			
DE	IG GAMMA-1 CHAIN C REGION.			
GN	IGH3L.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE: 82274238.			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma1 gene.";			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE: 71064024.			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RT	Waxdal M.J., Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";			
RN	Biochemistry 9:3161-3170(1970).			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE: 71064025.			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RT	Edelman G.M.;			
RL	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";			
RN	Biochemistry 9:3171-3181(1970).			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE: 77070269.			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The cytochrome peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE: 83289131.			
RA	Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE: 71064027.			
RA	Gall W.E., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. X. Intrachain disulfide bonds.";			

34	315.5	14.1	438	1	HVC2_HETFR	P23085 heterodontu
35	299	13.3	438	1	HVC3_HETFR	P23087 heterodontu
36	298	13.3	299	1	ALC_RABIT	P01879 oryctolagus
37	295	13.2	461	1	HVCB_HETFR	P23088 heterodontu
38	288	12.9	393	1	HVC3_HETFR	P23086 heterodontu
39	287.5	12.8	289	1	CD40_MOUSE	P27512 mus musculu
40	282.5	12.6	446	1	MUC_CHICK	P01875 gallus gall
41	279.5	12.5	370	1	HVC1_HETFR	P23084 heterodontu
42	277.5	12.4	353	1	ALC1_HUMAN	P01876 homo sapien
43	274.5	12.3	353	1	ALC1_GORGO	P20758 gorilla gor
44	273.5	12.2	340	1	ALC2_HUMAN	P01877 homo sapien
45	264	11.8	277	1	CD40_HUMAN	P25942 homo sapien

```

RL Biochemistry 9:3188-3196(1970).
RN [7]
RP DISULFIDE BONDS.
RX MEDLINE: 77070267.
RA Dieker L., Schwarz J., Reichel W., Hilschmann N.;
RT "Rule of antibody structure. The primary structure of a monoclonal
RT IgG1 immunoglobulin (myeloma protein Nie), I: Purification and
RT characterization of the protein, the L- and H-chains, the
RT chaperon bromide cleavage products, and the disulfide bridges.";
RT Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).
RL [8]
RN X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).
RP MEDLINE: 81208100.
RX Deisenhofer J.;
RT "Crystallographic refinement and atomic models of a human Fc fragment
RT and its complex with fragment B of protein A from Staphylococcus
RT aureus at 2.9- and 2.8-A-resolution.";
RT Biochemistry 20:2361-2370(1981).
-1- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPE MARKER, 97-K, & THE
-1- GJM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GJM(3)
-1- MARKER & THE GJM (NON-1) MARKERS.
-1- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF
-1- 35,116,198,269 & 272.
-1- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF
-1- 135, 166, 177, 193, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES
-1- 268-272.
-1- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF
-1- RESIDUES 198, 267&272.
-----
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CC
CC EMBL, J00228; AAC82527.1; ALT_INIT.
DR PIR; A02146; GHU.
DR PDB; 1FC1; 15-JUL-92.
DR PDB; 1FC2; 15-JUL-92.
DR MIM; 147100; -.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PIRAM; PF00047; 147; 3.
DR PROSITE; PS00290; IG_MHC; 2.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
DR 3D-structure.
FT NON_TER 1 1
FT DOMAIN 1 98
FT DOMAIN 99 110
FT DOMAIN 111 223
FT DOMAIN 224 330
FT DISULFID 27 83
FT DISULFID 103 103
FT DISULFID 109 109
FT DISULFID 112 112
FT DISULFID 144 204
FT DISULFID 250 308
FT CARBOHYD 180 180
FT VARIANT 97 97
FT VARIANT 239 239
FT VARIANT 241 241
FT MOD_RES 330 330
FT STRAND 123 126
FT HELIX 130 134
FT TURN 136 137
FT STRAND 141 148
FT STRAND 158 162
FT TURN 163 164
CH1.
HINGE.
CH2.
CH3.
INTERCHAIN (WITH LIGHT CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
INTERCHAIN (WITH HEAVY CHAIN).
N-LINKED (GICNAC. . .).
K -> R (IN GJM(3) MARKER).
/FTID-VAR_003886.
D -> E (IN GJM(NON-1) MARKER).
/FTID-VAR_003887.
L -> M (IN GJM(NON-1) MARKER).
/FTID-VAR_003888.
REMOVED POST-TRANSLATIONALLY.

```

Query Match	55.1%: Best Local Similarity	Score 1234: DB 1: Length 330:
Matches 232: Conservative	4: Mismatches	6: Indels 10: Gaps 2
FT STRAND	165	166
FT STRAND	175	178
FT STRAND	183	190
FT HELIX	193	197
FT TURN	198	199
FT STRAND	202	206
FT STRAND	215	219
FT STRAND	227	227
FT STRAND	230	234
FT HELIX	238	240
FT TURN	241	242
FT STRAND	245	256
FT STRAND	260	266
FT TURN	267	268
FT STRAND	269	270
FT STRAND	274	276
FT STRAND	280	281
FT TURN	283	284
FT STRAND	287	296
FT HELIX	297	301
FT TURN	302	303
FT STRAND	306	312
FT TURN	313	314
FT TURN	316	317
FT STRAND	320	324
FT SEQUENCE	330 AA; 36106 MW; 3770EB106C2FA3D CRC64;	

Query Match	55.1%	Score 1234;	DB 1;	Length 330;
Best Local Similarity	92.1%	Prod. No. 76-77;		
Matches 232;	Conservative	4;	Mismatches	6; Indels 10; Gaps
QY 159	THDNICS-----GNSESTQKV----	DKTHTCPCPAPABELLGGSVFLPPPKXDTLMIS	2068	
Db 78	TQTYICVNNHKSPTNWKYDKKEPKSCDKTHTCPCPABELLGGSVFLPPPKXDTLMIS	1377		
QY 209	RTPPEVTCVYVDVSHEDDEVKFNWYVDDEVVHNATKFRREQYNSTYVSVLTALHODWL	2666		
Db 138	RTPEPTCVYVDVSHEDDEVKFNWYVDDEVVHNATKFRREQYNSTYVSVLTALHODWL	1978		
QY 269	NGKEYKCKVSKNALPAPILEKTIKSKAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFY	328		
Db 198	NGKEYKCKVSKNALPAPILEKTIKSKAKGQPREPQVYTLPPSDELTKNQVSLTCLVKGFY	257		
QY 329	SDIAYEWESNQCPENNTKTPPVLDISGSEFFLYSKLTVDKSRMOQGVNFCSCVNHGLHN	388		
Db 258	SDIAYEWESNQCPENNTKTPPVLDISGSEFFLYSKLTVDKSRMOQGVNFCSCVNHGLHN	317		
QY 389	HYTQKSLSLSPG 400			
Db 318	HYTQKSLSLSPG 329			

RESULT 2	GC2_HUMAN	STANDARD;	PRT;	326 AA.
ID GC2_HUMAN				
AC P01859				
DT 21-JUL-1986 (Rel. 01, Created)				
DT 21-JUL-1986 (Rel. 01, Last sequence update)				
DT 15-JUL-1999 (Rel. 38, Last annotation update)				
DE IG GAMMA-2 CHAIN C REGION.				
DE IGHG2.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
LN [1]				
RP SEQUENCE FROM N.A.				
RX MEDLINE; 82197621.				
RA Ellison J.W., Hood L.E.;				
RT "Linkage and sequence homology of two human immunoglobulin gamma				
RT heavy chain constant region genes";				
FL Proc. Natl. Acad. Sci. U.S.A. 75:1984-1988(1982).				
LN [2]				

RP SEQUENCE OF 1-325 (MELOMA PROTEIN TIL).
 RX MEDLINE: 81007873.
 RA Wang A.-C., Tung E., Fudenberg H.R.;
 RT "The primary structure of a human IgG2 heavy chain: genetic,
 RL evolutionary, and functional implications.";
 RN J. Immunol. 125:1048-1054(1980).
 RP SEQUENCE OF 1-85 AND 132-325 (MELOMA PROTEIN ZIE).
 RX MEDLINE: 80001357.
 RA Connell G.E., Parr D.M., Hofmann T.;
 RT "The amino acid sequences of the three heavy chain constant region
 RL domains of a human IgG2 myeloma protein.";
 RN Can. J. Biochem. 57:758-767(1979).
 RP SEQUENCE OF 238-275 (ZIE).
 RX MEDLINE: 80114419.
 RA Hofmann T., Parr D.M.;
 RT "A note of the amino acid sequence of residues 381-391 of human
 RL immunoglobulin gamma chains";
 RN Mol. Immunol. 16:923-925(1979).
 RP REVISIONS TO 25, 59, 60 AND 264-268 (ZIE).
 RX MEDLINE: 80114419.
 RA Hofmann T., Parr D.M.;
 RT Submitted (MAR-1980) to the PIR data bank.
 RN [6]
 RP SEQUENCE OF 1-121 (DOT).
 RX MEDLINE: 95255298.
 RA Stopini M., Bellotti V., Negri A., Merlini G., Garver F., Ferri G.;
 RT "Characterization of the two unique human anti-flavin monoclonal
 RL immunoglobulins";
 RN Eur. J. Biochem. 228:886-893(1995).
 RP DISULFIDE BONDS.
 RX MEDLINE: 72033500.
 RA Milstein C., Frangione B.;
 RT "Disulphide bridges of the heavy chain of human immunoglobulin G2.";
 RN Biochem. J. 121:217-225(1971).
 RP DISULFIDE BONDS.
 RX MEDLINE: 69064124.
 RA Frangione B., Milstein C., Pink J.R.L.;
 RT "Structural studies of immunoglobulin G.";
 RN Nature 221:145-148(1969).
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 DR EMBL: V00554; CAA23814.1; -
 DR EMBL: V00554; CAA23815.1; -
 DR EMBL: V00554; CAA23816.1; -
 DR EMBL: V00554; CAA23817.1; -
 DR PIR: A02148; G2HU.
 DR MIM: 147110; -
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PIR: A02148; G2HU.
 DR PROSITE: PS00290; IG_MHC. 2.
 DR Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1 1
 FT DOMAIN 1 98
 FT DOMAIN 99 110
 FT DOMAIN 111 219
 FT DOMAIN 220 326
 FT DISULFID 14 14
 FT DISULFID 27 83
 FT DISULFID 102 102
 FT DISULFID 103 103
 FT DISULFID 106 106
 INTERCHAIN (WITH A LIGHT CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).
 INTERCHAIN (WITH A HEAVY CHAIN).

FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 140 200
 FT DISULFID 246 304
 FT VARIANT 60 60
 FT SITE 156 156
 FT MOD_RES 326 326
 SQ SEQUENCE 326 AA; 35884 MW; 8310878C6878CF9C CRC64;
 Query Match 51.3%; Score 1148.5; DB 1; Length 326;
 Best Local Similarity 90.3%; Pred. No. 4,2e-71;
 Matches 214; Conservative 8; Mismatches 8; Indels 7; Gaps 2;
 QY 170 STOKVDKT-----HICPPAPBELLGSPVFLPPPKKDTLMISRTPEVTVVDSHE 223
 Db 90 SNRKVDKVERKCCVCEPPCPAPP-VAGSPVFLFPPPKDTLMISRPEVTVVDSHE 148
 QY 224 DPEYKENVYDGYEVNNAKTRPREDOYNTYRYVSVTLVHOMLNGKEKCKVSNKALP 283
 Db 149 DPEVQFNWYDGVNNAKTRPREDOYNTYRYVSVTLVHOMLNGKEKCKVSNKGLP 208
 QY 284 APIEKTISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPEN 343
 Db 209 APIEKTISKAKGPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPEN 268
 QY 344 NYKTPPVLDSDGSFPLYSKLVDRKSRMOGNYFSCSVMEALHNHYTKSLSLSPG 400
 Db 269 NYKTPPVLDSDGSFPLYSKLVDRKSRMOGNYFSCSVMEALHNHYTKSLSLSPG 325
 RESULT 3
 GC4_HUMAN STANDARD; PRT; 327 AA.
 ID GC4_HUMAN
 AC P01861;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-4 CHAIN C REGION.
 GN IGHG4.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 83157104.
 RA Ellison J.W., Buxbaum J.N., Hood L.E.;
 RT "Nucleotide sequence of a human immunoglobulin C gamma 4 gene.";
 RL DNA 1:11-18(1981).
 RN [2]
 RP SEQUENCE OF 1-30 AND 81-326.
 RX MEDLINE: 70207560.
 RA Pink J.R.L., Buttery S.H., de Vries G.M., Milstein C.;
 RT "Human immunoglobulin subclasses. Partial amino acid sequence of the
 RL constant region of a gamma 4 chain.";
 RN Biochem. J. 117:33-47(1970).
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 CC
 DR EMBL: K01316; AAB59394.1; ALU_INIT.
 DR PIR: A02150; GAHU.
 DR MIM: 147130; -
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PIR: A02150; GAHU.
 DR PROSITE: PS00290; IG_MHC. 2
 DR Immunoglobulin domain; Immunoglobulin C region.
 KW

SEQUENCE 290 AA: 32331 MW: E69CB9C95705B2F46 CRC64;

Query Match
Best Local Similarity 70.8%; Pred. No. 3.8e-70;
Matches 218; Conservative 19; Mismatches 22; Indels 49; Gaps 5;

97 CLHNSC---PPGFGVYQACTPERNTVCKNCPDGFSTNETSKAP-CRKHTNSVFGLL 152
DB 27 CPEPKSCDTPPP-----CPRCPPEP-KSCDPPPCPPRCPPEPKSC----- 63

153 TQGNMTHDHCIGSNGSTOKVDKTHCPCPAPELLGGSVFLFPKPKDLMISRTPE 212
DB 64 -----DTPPCPCPPAPPELLGGSVFLFPKPKDLMISRTPE 101

213 VTCVVVDVSHEDPEVKENMYVDGVEVHNAKTKPREEQNTSYRVSALYTHLDOMLNGKE 272
DB 102 VTCVVVDVSHEDPEVKENMYVDGVEVHNAKTKPREEQNTSYRVSALYTHLDOMLNGKE 161

273 YKCKVSKKALPAPIEKTISKAKGQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIA 332
DB 162 YKCKVSKKALPAPIEKTISKAKGQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIA 221

333 VEMESNGOPENNYKTKTPPVYDSGSEFLYSKLTVDKSRMGOQNVFSCSVHREALHNHTQ 392
DB 222 VEMESNGOPENNYKTKTPPVYDSGSEFLYSKLTVDKSRMGOQNVFSCSVHREALHNHTQ 281

393 KSLSLSPG 400
DB 282 KSLSLSPG 289

RESULT 5
GC_RABIT STANDARD; PRT; 323 AA.
AC P01870:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA CHAIN C REGION.
OC Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
RN (1)
RP SEQUENCE FROM N.A.
RA Bernstein K.E., Alexander C.B., Mage R.G.;
RT "Nucleotide sequence of a rabbit IgG heavy chain from the recombinant
F-I haplotype."
RT Immunogenetics 18:387-397(1983).
RP (2)
RP SEQUENCE OF 1-128.
RX MEDLINE: 76135469.
RA Pratt D.M., Mole L.E.;
RT "Sequence studies on the constant region of the Fd sections of rabbit
immunoglobulin G of different allotype."
RT Biochem. J. 151:337-349(1975).
RN (3)
RP SEQUENCE OF 88-266 FROM N.A.
RX MEDLINE: 83299917.
RA Martens C.L., Moore K.W., Steilmetz M., Hood L., Knight K.L.;
RT "Heavy chain genes of rabbit IgG: Isolation of a cDNA encoding gamma
heavy chain and identification of two genomic C gamma genes."
RT Proc. Natl. Acad. Sci. U.S.A. 79:6018-6022(1982).
RN (4)
RP SEQUENCE OF 132-161.
RX MEDLINE: 70110015.
RA Fruchter R.G., Jackson S.A., Mole L.E., Porter R.R.;
RT "Sequence studies of the Fd section of the heavy chain of rabbit
immunoglobulin G."
RT Biochem. J. 116:249-259(1970).
RN (5)
RP SEQUENCE OF 129-131 AND 155-322.

RA Hill R.L., Lepovitz H.E., Fellows R.E. Jr., Delaney R.;
RL (in) Kiliander J. (eds.);
RL Gamma globulins, Nobel symp. 3, pp.109-127, Almqvist and Wiksell,
Stockholm (1967).
CC -1- MISCELLANEOUS: REF.1 SEQUENCE HAS THE D12 ALLOTYPIC MARKER,
CC 104-THR. AND THE E14 MARKER. 185-THR. REF.3 HAS THE D11 AND E15
CC MARKERS AND REF.5 THE E15 MARKER.
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CC
CC EMBL: M16426; AAA1289.1; -.
DR PIR: A02161; GHRB.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT VARIANT 104 104 T -> M (IN D11 MARKER).
FT VARIANT 185 185 T -> A (IN E15 MARKER).
FT CONFLICT 48 48 N -> E (IN REF. 2).
FT CONFLICT 71 71 V -> VPV (IN REF. 2).
FT CONFLICT 144 144 Q -> E (IN REF. 3 AND 4).
FT CONFLICT 173 173 N -> D (IN REF. 5).
FT CONFLICT 187 187 Q -> E (IN REF. 3 AND 5).
FT CONFLICT 201 201 N -> D (IN REF. 5).
FT CONFLICT 218 218 Q -> E (IN REF. 5).
FT CONFLICT 233 233 E -> Q (IN REF. 5).
FT CONFLICT 246 246 N -> D (IN REF. 5).
FT CONFLICT 256 256 E -> G (IN REF. 5).
FT CONFLICT 260 260 N -> D (IN REF. 5).
FT CONFLICT 266 266 N -> D (IN REF. 5).
FT CONFLICT 280 280 Y -> W (IN REF. 5).
FT CONFLICT 284 284 N -> S (IN REF. 5).
SO SEQUENCE 323 AA: 35404 MW: 69E8BA118D579A8B CRC64;

Query Match
Best Local Similarity 61.5%; Score 923; DB 1; Length 323;
Matches 177; Conservative 33; Mismatches 46; Indels 32; Gaps 5;

123 RCPDGFSS-----NETSKAPCKKHNCSVFGLLTKQGNATHDNCSGNSESTOKVDKT 177
DB 57 KQSSGLYSLSVSVSVTSSTSP-----VTCNV-----AHPATNTKVDKT 94

178 ---HTC--PPCPAPPELLGGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENMY 232
DB 95 VAPTSKTPCPPEPELLGGSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKENMY 154

233 VDCVEVHNAKTKPREEQNTSYRVSALYTHLDOMLNGEYKCKVSKKALPAPIEKTISK 292
DB 155 INNEQVTRAPPLREDOQFNSTIRVSTLPTTHODWLRGKFKCKVSKKALPAPIEKTISK 214

293 AKGQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTKTP 352
DB 215 AKGQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNYKTKTP 274

353 DSDGSEFLYSKLTVDKSRMGOQNVFSCSVHREALHNHTQKSLSLSPG 400
DB 275 DSDGSEFLYSKLTVDKSRMGOQNVFSCSVHREALHNHTQKSLSLSPG 322

RESULT 6
GC2_CAVPO STANDARD; PRT; 329 AA.
ID GC2_CAVPO
AC P01862;
DT 21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG GAMMA-2 CHAIN C REGION.
 OS Cavia porcellus (Guinea pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.
 RN [1]
 RP SEQUENCE OF 1-3.
 RA Trischmann T.M.;
 RL Submitted (APR-1975) to the PIR data bank.
 RN [2]
 RP SEQUENCE OF 4-68.
 RA MEDLINE; 71058471.
 RA Birshrein B.K., Hussain Q.Z., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 immunoglobulin-6(2). 3. Amino acid sequence of the region around the
 half-cysteine joining heavy and light chains.";
 RT Biochemistry 10:18-25(1971).
 RL [3]
 RP SEQUENCE OF 69-133 AND 312-329.
 RA MEDLINE; 71058486.
 RA Turner K.J., Cebra J.J.;
 RT "Structure of heavy chain from strain 13 guinea pig
 immunoglobulin-6(2). II. Amino acid sequence of the carboxyl-terminal
 and hinge region cyanogen bromide fragments.";
 RT Biochemistry 10:9-17(1971).
 RL [4]
 RP SEQUENCE OF 134-226.
 RA MEDLINE; 75036072.
 RA Tracey D.E., Cebra J.J.;
 RT "Primary structure of the CH2 homology region from guinea pig IgG2
 antibodies.";
 RT Biochemistry 13:4796-4803(1974).
 RL [5]
 RP SEQUENCE OF 227-311.
 RA MEDLINE; 75036073.
 RA Trischmann T.M., Cebra J.J.;
 RT "Primary structure of the CH3 homology region from guinea pig IgG2
 antibodies.";
 RT Biochemistry 13:4804-4811(1974).
 RL [6]
 RP DISULFIDE BONDS.
 RA MEDLINE; 71058474.
 RA Oliveira B., Lamm M.E.;
 RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin.";
 RT Biochemistry 10:26-31(1971).
 RL [7]
 RP MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
 13 INBRED GUINEA PIGS.
 RA PIR; A02151; G2GP.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM; PF00047; 19; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.
 FT NON_TER 1 1
 FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 28 79
 FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 142 202
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
 FT DISULFID 248 308
 FT SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;
 SQ
 Query Match 40.4%; Score 904.5; DB 1; Length 329;
 Best Local Similarity 60.3%; Pred. No. 1.4e-54;
 Matches 173; Conservative 30; Mismatches 53; Indels 31; Gaps 3;
 QY 127 GFSSNETSSKAPCRKHTNCSVFGILLTQGNATHDNICSGNSESTQKYDKT-----177
 DB 61 GLYSILTSVTVPSQKATCNV-----AHPASSTKVDKVEPIRTPZP 102

178 --HTCPBPAPBELLGSPVFLFPKPKDTIMISRTPEVTCVWVDVSHDEPEVKNWYDQ 235
 DB 103 BPCCTPCPCPPENLGGSVFIFPPKPKDTIMISTPEVTCVWVDVSDDEPEVQFTWVDN 162
 QY 236 VEVNATKTPREEOYNSTYRVSVLFTVHODWLNKGRKYSKALPAPIEKTIKSKAK 295
 DB 163 KPVGNATKPRVEQNTTFVESVLPFGHODWLNKGRKYSKALPAPIEKTIKSKAK 222
 QY 296 QPREOYTLPPSHDELTKNQVSLTCLVKGFYPSDIAVEESNQGP--ENNYKTPPVLD 353
 DB 223 APRAPDVYTLPPSHDELTKRSVYTCCLINFEFPADIVHVASNRPVSEKYEKNTPIED 282
 QY 354 SDGSFELYSKITVDSRWQGVSCVMEHALNHNHTOKSLSPG 400
 DB 293 ADGSYFLYSKITVDSKAMDGTVTYCSVMHEALNHNHTOKAISPSG 329
 RESULT 7
 GC3_MOUSE STANDARD; PRT; 329 AA.
 ID GC3_MOUSE
 AC P22436;
 DT 01-AUG-1991 (Rel. 19, Created)
 DT 01-AUG-1991 (Rel. 19, last sequence update)
 DT 15-JUL-1999 (Rel. 38, last annotation update)
 DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE; 85027161.
 RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
 RA Tucker P.W., Blattner P.R.;
 RT "Structural analysis of the murine IgG3 constant region gene.";
 RT EMBO J. 3:2041-2046(1984).
 RL
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 CC
 DR EMBL; J00451; -. NOT_ANNOTATED_CDS.
 DR PIR; B02156; G3MSC.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM; PF00047; 19; 3.
 DR PROSITE; PS00290; IG_MHC; 1.
 KW Immunoglobulin C region; glycoprotein; Transmembrane;
 KW Alternative splicing.
 FT NON_TER 1 1
 FT DOMAIN 1 97 CH1.
 FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 223 CH2.
 FT DOMAIN 224 327 CH3.
 FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;
 SQ
 Query Match 37.8%; Score 847.5; DB 1; Length 329;
 Best Local Similarity 54.0%; Pred. No. 9.7e-51;
 Matches 162; Conservative 47; Mismatches 72; Indels 19; Gaps 5;
 QY 107 FGVQAGTPERNVCKRCPGFFSNETSSKAPCRKHTNCSVFGILLTQGNATHDNICSG 166
 DB 42 YGALSSGV---RTVSVLQSGFVLSLVTVPSSTWPSQYI-----CNVAPR---AS 88
 QY 167 NSESTQKYD---KTHICP--PCPAPBELLGSPVFLFPKPKDTIMISRTPEVTCVWVDV 220
 DB 89 KTELIRIEPIRIPRSPSPSSCPGNIIGSPVFIIPPCKRDMISTLPKTYCVWVDV 148


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OY 221 SHEDPEVFNWYVDGEVHNATKPREBOYNSTYRVSVTLVHODMLNGEKYKCVSNK 280
DB 149 SEDDDPVHVSWEVDNKEVHTAWTQPREAOYNSTFRVVSALPIOHODMWRKEKCKVNNK 208
OY 281 ALPAPIEKTIKSAKAGPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDAEWMSNGC 340
DB 209 ALPAPIERISIKPKAGAPQVYTLPPRBOYKSKVSLTCLVNTFSEALSTWERNGE 268
OY 341 PENNYKTPPVLDSDGSFLLYSKLVYDKSRMOGNGVSCSVMEALHNHTQKSLSPG 400
DB 269 LRDYKNTPEPILDSDETYFLYSKLVYDTSWLOGEIFTCVSHVMEALHNHTQKSLSPG 328

```

RESULT 8

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GCB_RAT      STANDARD;      PRT;      333 AA.
ID GCB_RAT
AC 20761;
DT 01-FEB-1991 (rel. 17, Created)
DT 01-FEB-1991 (rel. 17, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
IG GAMMA-2B CHAIN C REGION.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
[1]
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR; PS0018; PS0018.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFM; PF00047; 19; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1
FT DISULFID 15
FT DISULFID 15
FT DISULFID 27
FT DISULFID 106
FT DISULFID 106
FT DISULFID 109
FT DISULFID 109
FT DISULFID 112
FT DISULFID 112
FT DISULFID 115
FT DISULFID 115
FT DISULFID 147
FT DISULFID 207
FT DISULFID 253
FT DISULFID 311
SO SEQUENCE 333 AA; 36497 MW; 55F8B64D48D460A6 CRC64;

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Query Match

Best Local Similarity 37.6%; Score 843; DB 1; Length 333;
Matches 161; Conservative 38; Mismatches 53; Indels 34; Gaps 4;

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OY 130 SNETSKRACRHRNCSVFGLLTOKGNATHDNICGNSSESTOKVDKT-----HTC 180
DB 66 SSVTSSTWSPQVVT-CNV-----AHASSIKVDKVERNRNGSIGHC 106
OY 181 P-----PCPAPELLGSPVFLPPKPKDTLMISRPETCVYVDVSHEDPEKFNWYVD 234
DB 107 PCPCPTCHKCPVPELLGSPVFLPPKPKDILLISONAKVTCVAVDSEEDPDQFSWFVN 166
OY 235 GVEVHNATKPREBOYNSTYRVSVTLVHODMLNGEKYKCVSNKALPAPIEKTIKSAK 294
DB 167 GVEVHTAQTQPREBOYNSTFRVVSALPIOHODMWSKEKCKVNNALSPLEKTIKSKR 226
OY 295 GPREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDAEWMSNGCPENNYKTPPVLD 354
DB 227 GLVAKQVYVWGPPTQLEQVYSLTCLNGSGLPNDIGVEMTNGHIEKNKTEBEVMD 286
OY 355 DGSFLLYSKLVYDKSRMOGNGVSCSVMEALHNHTQKSLSPG 400
DB 287 DGSFLLYSKLVYDKSRMOGNGVSCSVMEALHNHTQKSLSPG 332

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RESULT 9

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GCB_MOUSE     STANDARD;      PRT;      398 AA.
ID GCB_MOUSE
AC P03987;
DT 23-OCT-1986 (rel. 02, Created)
DT 01-AUG-1991 (rel. 19, Last sequence update)
DT 15-JUL-1999 (rel. 38, Last annotation update)
IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85027161.
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine Ig3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE; 84041483.
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
RA Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
CC -----
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CC -----
DR EMBL; J00451; AAB59655.1; -.
DR EMBL; J01526; CAA24767.1; ALT_SEQ.
DR PIR; A02155; G3MSM.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFM; PF00047; 19; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Transmembrane; Alternative splicing.
FT NON_TER 1
FT DOMAIN 1
FT DOMAIN 97
FT DOMAIN 98
FT DOMAIN 113
FT DOMAIN 114
FT DOMAIN 223
FT DOMAIN 224
FT DOMAIN 327
FT TRANSMEM 346
FT TRANSMEM 362
FT DOMAIN 363
FT DOMAIN 363
FT DOMAIN 398
FT CONFLICT 342
FT CONFLICT 342
FT CONFLICT 382
FT CONFLICT 388
SO SEQUENCE 398 AA; 43929 MW; CFF7264B50A1B95 CRC64;

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Query Match

Best Local Similarity 37.6%; Score 841.5; DB 1; Length 398;
Matches 161; Conservative 47; Mismatches 72; Indels 19; Gaps 5;

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OY 107 FGVOAGIPERTVTCRCPDGFSSNETSKRACRHRNCSVFGLLTOKGNATHDNICSG 166
DB 42 YGALSSGV---RTVSSVLSQSGFYSLSLVTPYPSSTWSPQVY-----CNVAHP---AS 88
OY 167 NSESQKVD---KTHGPC--PCPAPELLGSPVFLPPKPKDTLMISRPETCVYVDV 220
DB 89 KTELKRIEPRPKSTPSPGSCPPCNILGGSVIFPPKPKDALMISLTKRYTCVYVDV 148
OY 221 SHEDPEVFNWYVDGEVHNATKPREBOYNSTYRVSVTLVHODMLNGEKYKCVSNK 280
DB 149 SEDDDPVHVSWEVDNKEVHTAWTQPREAOYNSTFRVVSALPIOHODMWRKEKCKVNNK 208

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QY 281 ALPAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSYDAVWESNGQ 340
DB 209 ALPAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSYDAVWESNGE 268
QY 341 PENNYKTPPEVLDSGSEFFLYSKLTVDKSRMOQGVSCSVMEALHNHYTOKSLSP 399
DB 269 LEQDYKNTPTILSDGTYFLYSLKLTVDTSWLMGSEIFTCVSHALNHNHTOKLSNSP 327

RESULT 10
GCL_MOUSE STANDARD: PRT: 324 AA.
ID GCL_MOUSE
AC P01868:
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 80045036.
RA Horio T., Ohta M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
RA Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene."
RL Cell 18:559-568 (1979).
[2]
RN SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RA Ohta M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
RA Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid."
RL Gene 9:87-97 (1980).
[3]
RN SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RA MEDLINE: 80012837.
RA Rogers J., Clarke P., Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain."
RL Nucleic Acids Res. 6:3305-3321 (1979).
[4]
RN SEQUENCE (MYELOMA PROTEIN MOPC 21).
RP MEDLINE: 78242288.
RA Adetugbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain."
RL J. Biol. Chem. 253:6068-6075 (1978).
[5]
RN DISULFIDE BONDS (MOPC 21).
RX MEDLINE: 73008889.
RA Svasti J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RL Biochem. J. 126:837-850 (1972).
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CC
CC EMBL: V00793; CAA24172.1; -
CC EMBL: V00793; CAA24173.1; -
CC EMBL: V00793; CAA24174.1; -
CC EMBL: V00793; CAA24175.1; -
CC EMBL: V00793; CAA24176.1; -
CC PIR: A02159; GIMS.
CC MGD: MGI:96446; IGH-4.
CC INTERPRO: IPR000495; -

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DR INTERPRO: IPR003006; -.
DR PRAM: PR00047; 1g: 3.
DR PROSITE: PS00290; IG_MHC, 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97
FT DOMAIN 98 110
FT DOMAIN 111 217
FT DOMAIN 218 324
FT DISULFID 27 82
FT DISULFID 102 102
FT DISULFID 104 104
FT DISULFID 107 107
FT DISULFID 109 109
FT DISULFID 138 198
FT CARBOHYD 174 174
FT MOD_RES 244 302
FT MOD_RES 324 324
FT CONFLICT 276 276
FT CONFLICT 278 278
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1FC093 CRC64;

Query Match 36.6%; Score 820; DB 1; Length 324;
Best Local Similarity 60.5%; Pred. No. 6; 9e-49;
Matches 144; Conservative 45; Mismatches 39; Indels 10; Gaps 3;

QY 170 STQKVDKTHT----CPP--CPAPELLGSPVFLPPPKKDTIMISRTPEVTCVVDVSH 222
DB 89 SSTKVKRKIVPRDCKGCKPCICTVPEV---SSVFIFPKPKRDVLTITLTKVTCVVDISK 145
QY 223 EDEEVFNMYDVEVHNKTRREDOYNSTYRVSVLVLYHODMNGREYKCKVSNKL 282
DB 146 DDEVOGSMFVDVEVHTAQTPREDOFNSTFRSVSELPIMHODMNGKFKCKVSAAP 205
QY 283 PAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSYDAVWESNGQPE 342
DB 206 PAPIETKISKAKGPREPOVYTLPPSRDELTKNOVSLCIYKGFPSYDAVWESNGE 265
QY 343 NNTKTPPEVLDSGSEFFLYSKLTVDKSRMOQGVSCSVMEALHNHYTOKSLSPG 400
DB 266 ENYKNTQPIMTNGSYFYVSKLVNOKSNMEAGNTFTCSVLHGLHNHHTKSLSPG 323

RESULT 11
GCL_RAT STANDARD: PRT: 326 AA.
ID GCL_RAT
AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
RN [1]
RN SEQUENCE FROM N.A.
RP MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family."
RL Gene 74:473-482 (1988).
RL PIR: PS0017; PS0017.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g: 3.
DR PROSITE: PS00290; IG_MHC, 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DOMAIN 1 97
FT DOMAIN 98 112
FT DOMAIN 113 219
FT DOMAIN 220 326
FT CH1.
FT HINGE.
FT CH2.
FT CH3.

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P01863;
 AC 21-JUL-1986 (Rel. 01, Last Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, A ALLELE.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81076554.
 RA Skora J. L., Auffray C., Rougeon F.;
 RT Structure of the constant and 3' untranslated regions of the murine
 RT Balb/c gamma 2a heavy chain messenger RNA.";
 RT Nucleic Acids Res. 8:3143-3155(1980).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81198976.
 RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
 RT The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
 RT and evolution of heavy chain genes: further evidence for intervening
 RT sequence-mediated domain transfer.";
 RT Nucleic Acids Res. 9:1365-1381(1981).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 81223894.
 RA Ojio R., Auffray C., Morchamps C., Rougeon F.;
 RT Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
 RT suggests that exons can be exchanged between genes in a multigenic
 RT family.";
 RT Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
 RN [4]
 RP MYELOMA PROTEIN MOPC 173.
 RX MEDLINE; 74175517.
 RA Bourgois A., Fougereau M., Rocca-Serra J.;
 RT Determination of the primary structure of a mouse IgG2a
 RT immunoglobulin: amino-acid sequence of the FC fragment. Implications
 RT for the evolution of immunoglobulin structure and function.";
 RT Eur. J. Biochem. 30:452-462(1972).
 RN [5]
 RP DISULFIDE BONDS.
 RX MEDLINE; 73056887.
 RA de Preval C., Fougereau M.;
 RT Determination of the primary structure of a mouse gamma G2a
 RT immunoglobulin. Identification of the disulfide bridges.";
 RT Eur. J. Biochem. 30:452-462(1972).
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 CC
 CC EMBL: V00798; CAA24178.1; -
 CC PIR: A02152; G2MSA.
 CC INTERPRO: IPR000495; -
 CC INTERPRO: IPR003006; -
 CC PIR: PF00047; 1g; 3.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region.
 KW NON_TER 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 250 308
 FT MOD_RES 330 330 REMOVED POST-TRANSLATIONALLY.
 FT SEQUENCE 330 AA; 36389 MW; B84361C545A6864 CRC64;

Query Match 36.3%; Score 812.5; DB 1; Length 330;
 Best Local Similarity 56.5%; Pred No. 2,3e-48;
 Matches 137; Conservative 34; Mismatches 58; Indels 29; Gaps 4;
 QY 133 TSSKAPCRKRTNCSVEGLLTLTKGNATHDNICGNSBSTOKYDK-----THTCPP--182
 DB 71 TSSWTFPSGQIT-CNV-----AHPASSTKVKKIKIEPRGRTIKPCKPCK 111
 QY 183 CPAPELLGSPSVFLFPKPKDTLMISTPEVTCVVDVSHEDPEVFNWYVDQVEYHNK 242
 DB 112 CPAPNLLGGSPVFLFPKIDVLMISLPITCVVDVSDDDVDQVLSWFNNEVHTAQ 171
 QY 243 TKPEEDQNTSTYRVSVLTGLHODWLNGKEYKCKSVSKALPAIEKTIISKAKGPREPV 302
 DB 172 TQTHREDYNTLKVSVLPLQHDQMSGKFEKCKVNNKDLPAIEKTIISKPKSVAPQV 231
 QY 303 YLPPEPHELTKNQVSLTCLVKGFPSPDIAVWESNGQPENNYKTPPVLDSDGSEFFLYS 362
 DB 232 YLPPEPEETKQVTLTQVTFDPEPEDIYVETWNTNGKETELNKPTEPLVDSGYFMY 291
 QY 363 KLYDKRMOQGVNFSGVNHEALNHYTKSLSPG 400
 DB 292 KLYEKKWVERNSYSCVYHGLHNNHTTKSPSPG 329
 RESULT 14
 GCAM_MOUSE STANDARD; PRT; 399 AA.
 ID GCAM_MOUSE
 AC P01865;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 01-AUG-1991 (Rel. 19, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2A CHAIN C REGION, MEMBRANE-BOUND FORM.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 82222190.
 RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
 RT Nucleotide sequences of gene segments encoding membrane domains of
 RT immunoglobulin gamma chains.";
 RT Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).
 CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
 CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
 CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
 CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
 CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
 CC SEGMENT OF MU CHAINS.
 CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
 CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
 CC THE A ALLELE.
 CC
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 CC
 CC EMBL: J00471; AAB59661.1; ALT_INIT.
 CC PIR: A02154; G2MSAM.
 CC MGD; MGI:96443; IGH-1.
 CC INTERPRO: IPR000495; -
 CC INTERPRO: IPR003006; -
 CC PIR: PF00047; 1g; 3.
 CC PROSITE: PS00290; IG_MHC; 1.
 CC Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
 KW Transmembrane; Alternative splicing.
 FT NON_TER 1 1
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).

FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 144 204
 FT DISULFID 250 308
 FT TRANSMEM 346 363
 FT DOMAIN 364 399
 FT CARBOHYD 180 180
 FT SEQUENCE 399 AA; 44020 MW; 4C38138BFAED3FF0 CRC64; POTENTIAL.
 N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 36.3%; Score 812.5; DB 1; Length 399;
 Best Local Similarity 56.5%; Pred. No. 2.8e-48;
 Matches 157; Conservative 34; Mismatches 58; Indels 29; Gaps 4;

QY 133 TSSKAPCRKHTNCVFGLLTKQKNATHNDCNSENSTQYDK-----THTCP-- 182
 DB 71 TSSWPSQST-CNV-----AHPASTVYDKKIEPRGPTIRPCPPCK 111
 QY 183 CPABELLGGPSVLEPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDVGVEVNAK 242
 DB 112 CPANLLGGPSVLEPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDVGVEVNAK 171
 QY 243 TKPREEDYNSTYRVSVLTVLHODMLNGKCKVSKNALPAPLEKTSKAKGP 302
 DB 172 TQHREEDYNSTYRVSVLTVLHODMLNGKCKVSKNALPAPLEKTSKAKGP 231
 QY 303 YLPPEDELTKNQVSLTCLVKGFPSPDIAMWESNGPENNKTTPVLDSDSFLYS 362
 DB 232 YLPPEDELTKNQVSLTCLVKGFPSPDIAMWESNGPENNKTTPVLDSDSFLYS 291
 QY 363 KLYVDSKRMQOGNFCVSMHEALHNHYTKSLSPG 400
 DB 292 KLYVDSKRMQOGNFCVSMHEALHNHYTKSLSPG 329

RESULT 15

GCC_RAT ID GCC_RAT STANDARD; PRT; 329 AA.

AC P20762;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-2C CHAIN C REGION.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 SEQUENCE FROM N.A.
 MEDLINE: 88166903.
 RA Brueggemann M., Delmastro-Galfre P., Waldmann H., Calabi F.;
 RT "Sequence of a rat immunoglobulin gamma 2c heavy chain constant
 region cDNA: extensive homology to mouse gamma 3.";
 RL Eur. J. Immunol. 18:317-319(1988).
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 CC
 DR EMBL: X07189; CAA30169.1; -
 DR PIR: S00847; S00847.
 DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PRAM: PF00047; 19; 3.
 DR PROSITE: PS00290; IG_MHC; 1.
 KW Immunoglobulin domain; Immunoglobulin C region.
 FT NON_TER 1
 FT DOMAIN 1 97 CH1.

FT DOMAIN 98 113 HINGE.
 FT DOMAIN 114 222 CH2.
 FT DOMAIN 223 329 CH3.
 FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 27 82 INTERCHAIN (WITH A LIGHT CHAIN).
 FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
 FT DISULFID 143 203
 FT DISULFID 249 307
 FT SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 35.9%; Score 804.5; DB 1; Length 329;
 Best Local Similarity 63.7%; Pred. No. 7.9e-48;
 Matches 142; Conservative 41; Mismatches 37; Indels 3; Gaps 1;

QY 181 PP--CPABELLGGPSVLEPPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYDVGVE 237
 DB 106 PPIDICSDNDLGRPSVFIFPPPKPKDTLMITLPKYTCVVDVSEEDPVQSFMYDNR 165
 QY 238 VNAKTRPREEDYNSTYRVSVLTVLHODMLNGKCKVSKNALPAPLEKTSKAKGP 297
 DB 166 VFTKOTQPHEDQNGTFRVYSTLIHQHODMWSGKCKVNNKDLPSPIKTSKPRGA 225
 QY 298 REQVYTLPSRDELTKNQVSLTCLVKGFPSPDIAMWESNGPENNKTTPVLDSDS 357
 DB 226 RTPGVYTLIPPREDSKNNKSLTCLVMSFYFASISVEMENGEEDQYKNTLPVLDSDS 285
 QY 358 FFLSKLTVDSKRMQOGNFCVSMHEALHNHYTKSLSPG 400
 DB 286 YFLSKLTVDSKRMQOGNFCVSMHEALHNHYTKSLSPG 328

Search completed: December 27, 2000, 10:55:07
 Job time: 209 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:52:38 ; Search time 60.82 Seconds
(without alignments)
614.102 Million cell updates/sec

Title: US-09-389-545-5

Perfect score: 2240
Sequence: 1 ETTPPKYLAHDETSNQLC.....VMHEALHNHYTKSLSPG 400

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Total number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: SP-REMBL_14:*
2: SP-archaea:*
3: SP-fungi:*
4: SP-human:*
5: SP-invertebrate:*
6: SP-mammal:*
7: SP-mhc:*
8: SP-organelle:*
9: SP-phage:*
10: SP-plant:*
11: SP-rodent:*
12: SP-virus:*
13: SP-vertebrate:*
14: SP-unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1013.5	45.2	401	4 000300	000300 homo sapien
2	1013	45.2	372	4 090HPA	090HPA homo sapien
3	893.5	39.9	401	11 008712	008712 mus musculu
4	877	39.2	401	11 008727	008727 ratus norv
5	827	36.9	437	11 09R1A4	09R1A4 mus musculu
6	433	19.3	300	4 095407	095407 mus musculu
7	405.5	18.1	302	13 09PUS0	09PUS0 salvelinus
8	345	15.4	459	11 062327	062327 mus musculu
9	343.5	15.3	439	4 016042	016042 homo sapien
10	338	15.1	482	11 088734	088734 mus musculu
11	297	13.3	655	4 075509	075509 homo sapien
12	280.5	12.5	684	13 090544	090544 ginsjymosto
13	277.5	12.4	384	4 09P60	09P60 homo sapien
14	258.5	11.5	616	4 09Y608	09Y608 homo sapien
15	236.5	11.5	625	11 035305	035305 mus musculu
16	241	10.8	349	12 057099	057099 monkeypox v
17	239	10.7	349	12 057291	057291 monkeypox v
18	239	10.7	349	12 057100	057100 monkeypox v
19	239	10.7	349	12 057101	057101 monkeypox v

20	239	10.7	349	12 057102	057102 monkeypox v
21	235.5	10.5	348	12 057277	057277 monkeypox v
22	235.5	10.5	348	12 057103	057103 monkeypox v
23	235.5	10.5	348	12 057108	057108 monkeypox v
24	229	10.2	348	12 057112	057112 variola vir
25	229	10.2	348	12 085407	085407 variola vir
26	226.5	10.1	349	12 057284	057284 camelipox vi
27	226.5	10.1	349	12 057098	057098 camelipox vi
28	226	10.1	349	12 057110	057110 variola vir
29	226	10.1	349	12 057111	057111 variola vir
30	226	10.1	349	12 089118	089118 variola vir
31	226	10.1	349	12 089098	089098 variola vir
32	223	10.0	350	12 057116	057116 cowpox viru
33	222.5	9.9	349	12 057097	057097 camelipox vi
34	222.5	9.9	350	12 057123	057123 cowpox viru
35	222.5	9.9	355	12 085308	085308 cowpox viru
36	221	9.9	349	12 057109	057109 variola vir
37	220.5	9.8	349	12 057305	057305 cowpox viru
38	219	9.8	326	12 057122	057122 cowpox viru
39	218.5	9.8	360	12 057118	057118 cowpox viru
40	217.5	9.7	326	12 057120	057120 cowpox viru
41	217.5	9.7	351	12 073559	073559 cowpox viru
42	216.5	9.7	351	12 057117	057117 cowpox viru
43	212.5	9.5	347	12 057115	057115 cowpox viru
44	210.5	9.4	316	12 057092	057092 ectromelia
45	210.5	9.4	320	12 057300	057300 ectromelia

ALIGNMENTS

RESULT	ID	AC	ID	AD	PRELIMINARY:	PRT:	401 AA.
000300	000300	060236					
01-JUL-1997	01-JUL-1997	(TREMBLrel. 04, Created)					
01-JUL-1997	01-JUL-1997	(TREMBLrel. 04, last sequence update)					
01-MAY-2000	01-MAY-2000	(TREMBLrel. 13, last annotation update)					
OSTEOBLAST PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)							
(OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).							
TNFRSF11B OR OPG OR OCIF.							
Homo sapiens (Human).							
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;							
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.							
[1]							
SEQUENCE FROM N.A.							
TISSUE=KIDNEY;							
MEDLINE: 97262071.							
Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,							
Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,							
Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,							
Davey E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,							
Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,							
Suags S., Boyle W.J.;							
"Osteoprotegerin: a novel secreted protein involved in the regulation							
of bone density."							
Cell 89:309-319(1997).							
[2]							
SEQUENCE FROM N.A.							
TISSUE=LUNG FIBROBLAST;							
MEDLINE: 98151033.							
Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,							
Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,							
Tsuda E., Morinaga T., Higashio K.;							
"Identity of osteoclastogenesis inhibitory factor (OCIF) and							
osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits							
osteoclastogenesis in vitro."							
Endocrinology 139:1329-1337(1998).							
[3]							
SEQUENCE FROM N.A.							
TISSUE=PLACENTA;							
MEDLINE: 98351569.							
Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;							

Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor;
 Eur. J. Biochem. 254:685-691(1998).
 -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
 -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB002146; BAA25910.1; -
 DR EMBL: AB008822; BAA32076.1; -
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1; -
 DR HSSP: P25942; ICDF.
 DR MIM: 602643; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 183 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 152 152 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
 SQ SEQUENCE 401 AA; 4596 MW; EB42FA51CD7C71E CRC64;

Query Match 45.2%; Score 1013.5; DB 4; Length 401;
 Best Local Similarity 68.7%; Pred. No. 4.5e-81;
 Matches 193; Conservative 12; Mismatches 37; Indels 39; Gaps 5;

QY 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKKTKVCAPCPDHYTDSWHTSDECL 60
 DB 22 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKKTKVCAPCPDHYTDSWHTSDECL 81
 QY 61 YCSPVCKELOYVQECNRTHNRYCECKEGRYLEIEFLKHSRCPGFGVVOAGTPRNTV 120
 DB 82 YCSPVCKELOYVQECNRTHNRYCECKEGRYLEIEFLKHSRCPGFGVVOAGTPRNTV 141
 QY 121 CKRCPDGFFENETSSKAPCKRHTNCSVFGLLLQKGNATHDNICSGNSESTOKVDTHTC 180
 DB 142 CKRCPDGFFENETSSKAPCKRHTNCSVFGLLLQKGNATHDNICSGNSESTOK 194
 QY 181 PRCPPAPLLGSPVFLPPRPKDTLMISRPVYTCVVDVSHDEPEYKFMVYDGVYHN 240
 DB 195 --CGIDVTLCEEAFFRPVAPTK-----FTPNMLSVLD-----NLPGRKYNA 234
 QY 241 AKTRPREOYNSTYRVSVTLVHQLDNLNGKEYCKYSNKA 281

DB 235. ESEYRIKROHSSQEQTFQLLKL-----KHQNK 263

RESULT 2
 Q9UHP4 PRELIMINARY; PRT; 372 AA.
 AC Q9UHP4;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE OSTEOPROTEGERIN (FRAGMENT).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
 DR EMBL: AF134187; AAF20168.1; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CDD3 CRC64;

Query Match 45.2%; Score 1013; DB 4; Length 372;
 Best Local Similarity 73.4%; Pred. No. 4.5e-81;
 Matches 190; Conservative 10; Mismatches 35; Indels 24; Gaps 5;

QY 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKKTKVCAPCPDHYTDSWHTSDECL 60
 DB 1 ETPPPKYLHDEETSHQLCDKCPGGTYLKQCTAKKTKVCAPCPDHYTDSWHTSDECL 60
 QY 61 YCSPVCKELOYVQECNRTHNRYCECKEGRYLEIEFLKHSRCPGFGVVOAGTPRNTV 120
 DB 61 YCSPVCKELOYVQECNRTHNRYCECKEGRYLEIEFLKHSRCPGFGVVOAGTPRNTV 120
 QY 121 CKRCPDGFFENETSSKAPCKRHTNCSVFGLLLQKGNATHDNICSGNSESTOKVDTHTC 180
 DB 121 CKRCPDGFFENETSSKAPCKRHTNCSVFGLLLQKGNATHDNICSGNSESTOK 173
 QY 181 PRCPPAPLLGSPVFLPPRPKDTLMISRPVYTCVVDVSHDEPEYKFMVYDGVYHN 240
 DB 174 --CGIDVTLCEEAFFRPVAPTK-----FTPNMLSVLD-----NLPGRKYNA 217
 QY 241 AKTRPREOYNSTYRVSV 259
 DB 218 -RIKROHSSQEQTFQLLKL 235

RESULT 3
 Q08712 PRELIMINARY; PRT; 401 AA.
 AC Q08712; 070202;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=KIDNEY;
 RX MEDLINE: 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,

[illegible]

FT	VARIANTNM	296	296	L > R (IN STRAINS 129/OLA AND NIH SWISS)
SO	SEQUENCE	401 AA;	45923 MM;	CNA0102DJB3J12470 CRC64;
Query Match		39.9%;	Score 893.5;	DB 11; Length 401;
Best Local Similarity		47.8%;	Pred. 1.5e-70;	
Matches 191;	Conservative 35;	Mismatches 107;	Indels 67;	Gaps
OY	1	ETPPKYLHVDENYSHOILCDKCPPGTYLKHONCTAKMTVCAPCPDHYYTDSMHTSDECL	60	
Db	22	ETLPKKYLNHPPEIGHOLLDDCKAPGYLLKHQHTVARKTLCPVCPPHSTSDSMHTSDEV	81	
OY	61	YCSPVKELQVYKOEKNRTHNRVCECKEGRYLEIEFQLKHSRCPCGFGVYAQTPERNTV	120	
Db	82	YCSPVKELOSVKOECKNRTNHRVCEGEGRYLEIEFCLKHSRCPCSGGVYAQTGERNTV	141	
OY	121	CKRPDDGFSEMSRSKAPCKRHNCVSFGLLNOKNATHNDNCNSNSRSTOKVNDKTHC	180	
Db	142	CKKCPDGFFSESTSKAPCIKHTNCSFGILLIQKGNATHDNVCSGNREATOR	194	
OY	181	PPCAPPELLGGPSVFLEPPPKPDKTLMISRPETYCVVVDSHEDPVKKFNWYVDGEVAN	240	
Db	195	--CGIDVTLCSEAEPFRRAVPTR-----IIPNLSTLYD---SLPSTKYN--AESYE---	238	
OY	241	AKTREPBEQYNSTRVYVSVLTVLHDQMLNGKEY-----KCKVS-----	278	
Db	239	-RIKRSHSSQOTPOLKLKMHQNRODEMVKRLIIDIDCESSVRHLGSM/LTEOLLA	297	
OY	279	-----NKALPALETITISKAGQPREPYVTL----PPSRDELTKNOVSLTCLYKGFY	327	
Db	298	LMESLPKGKIKSPIEIEITRTKTSKSSDLKLKLSLRMIKNGDDDTLKGLMYALKHLKTSHF	357	
OY	328	PSDIAVEWSNGCPENNYKTPPLVLDSDGSFYFSKLYVD	367	
Db	358	PKTVT-----HSLRKTMRFILHSFTMYRLQYKLFLE	387	
RESULT	4			
ID	008727	PRELIMINARY;	PRT:	401 AA.
AC	008727;			
DT	01-JUL-1997 (TREMblrel. 04, Created)			
DT	01-JUL-1997 (TREMblrel. 04, Last sequence update)			
DT	01-MAY-2000 (TREMblrel. 13, last annotation update)			
DE	OSTEOCYTOGENESIS PRECURSOR (OSTEOCYTOGENESIS INHIBITORY FACTOR) (OCIF).			
OS	TNFRSF1B OR OPG.			
OS	Rattus norvegicus (Rat).			
OC	Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;			
CC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=TESTINE;			
RX	MEDLINE: 97262071.			
RA	Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,			
RA	Leachy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,			
RA	DeRose M., Elliott R., Colombero A., Tan H.-L., Trail G., Shivanian J.,			
RA	Davy E., Bucay N., Renshaw-degg L., Hughes T.M., Hill D., Pettison W.,			
RA	Campbell P., Sander S., Van G., Tarpley J., Detty P., Lee R.,			
RT	Suggs S., Boyle W.J.;			
RT	"osteoprotegerin": a novel secreted protein involved in the regulation			
RT	of bone density.";			
RL	Cell 89:309-319(1997).			
CC	-!- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGE			
CC	OF OSTEOBLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY			
CC	SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO			
CC	OSTEOCYTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN			
CC	STROMAL CELLS AND OSTEOCLAST PROGENITORS.			
CC	-!- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM). (BY			
CC	SIMILARITY).			
CC	-!- SUBCELLULAR LOCATION: EXTRACELLULAR.			
CC	-!- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.			

DR EMBL: U94330; AAB53707.1; -
 DR HSSP: P25942; ICDF
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KM Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT SEQUENCE 401 AA; 46192 MW; FEC6A31FID4E573A CRC64;

Query Match 39.2%; Score 877; DB 11; Length 401;
 Best Local Similarity 63.7%; Pred. No. 4.2e-69;
 Matches 165; Conservative 18; Mismatches 52; Indels 24; Gaps 5;

OY 1 ETPPKYIHYDEBSHOLCDKCPGTYLKQCTAKMTVCAPCDHYTTSMTSDCL 60
 DB 22 ETPPKYIHYDEBSHOLCDKCPGTYLKQCTAKMTVCAPCDHYTTSMTSDCL 81
 OY 61 YCSPVCKELQYVQKCNTHNRVCECKEGRYLEIFECCKHSCPPGFGVVOAGPERMTY 120
 DB 82 YCSPVCKELQYVQKCNTHNRVCECKEGRYLEIFECCKHSCPPGFGVVOAGPERMTY 141
 OY 121 CKRCPDGFSESTSKACRKHNTGSGVGLLTOKGNTHDNIGSGNSESTOKYDKTHTC 180
 DB 142 CKRCPDGFSESTSKACRKHNTGSGVGLLTOKGNTHDNIGSGNSESTOKYDKTHTC 194
 OY 181 PRCAPBELGSPVFLPPPKRDTLMISRTPEYCVVVDVSHEDPEVFNMTVDGEVHN 240
 DB 195 --CGIDVTLCEAFRFVAVPTK-----TIPNWLSLVD---SLPGTRVN--AESVE--- 238
 OY 241 AKTRPREQYNTYRVAVS 259
 DB 239 -RIKRHSOSQOTFOLKL 256

RESULT 5
 O9RIA4 PRELIMINARY; PRT; 437 AA.
 AC O9RIA4
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, Last annotation update)
 DE GAMMAL HEAVY CHAIN OF MAB7 (FRAGMENT).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Wilde K.C., Yu X., Ekramoddoullah A.K.M., Misra S.;
 RT Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
 RT antibody (Mab 7, its light and heavy chains) and construction of a
 RT single chain antibody (scFv).
 RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF152372; AAD40243.1; -

DR INTERPRO: IPR000495; -
 DR INTERPRO: IPR003006; -
 DR PFAM: PF00047; IG; 4.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
 FT NON_TER 1 1
 FT NON_TER 437 437
 KM SEQUENCE 437 AA; 48142 MW; 5C3A7B33E7D697C CRC64;

Query Match 36.9%; Score 827; DB 11; Length 437;
 Best Local Similarity 60.9%; Pred. No. 1.1e-64;
 Matches 145; Conservative 44; Mismatches 39; Indels 10; Gaps 3;

OY 170 STQVVDKHT-----CPP--CPABELLGSPVFLPPPKRDTLMISRTPEYCVVVDVSH 222
 DB 202 STQVVDKHT-----CPP--CPABELLGSPVFLPPPKRDTLMISRTPEYCVVVDVSH 258
 OY 223 EDPVKKFMYVDGVEVNAKTRPREQYNTYRVAVSLTVLHODMLNGKCKRYSKAL 282
 DB 259 DDPVKKFMYVDGVEVNAKTRPREQYNTYRVAVSLTVLHODMLNGKCKRYSKAL 318
 OY 283 PAPLEKTSKAKGQPREQYNTYRVAVSLTVLHODMLNGKCKRYSKAL 342
 DB 319 PAPLEKTSKAKGQPREQYNTYRVAVSLTVLHODMLNGKCKRYSKAL 378
 OY 343 NNYKTPVLDSGSPFLYSKLTVDKSRMOGCVFSGVHNEALHNHYTOKSLSPG 400
 DB 379 ENYKTPVLDSGSPFLYSKLTVDKSRMOGCVFSGVHNEALHNHYTOKSLSPG 436

RESULT 6
 O95407 PRELIMINARY; PRT; 300 AA.
 AC O95407
 DT 01-MAY-1999 (TREMblrel. 10, Created)
 DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE DECOY RECEPTOR 3.
 GN DCR3 OR TR6.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 99087326.
 RA Pitti R.M., Masters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
 RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
 RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
 RA Goddard A.D., Botstein D., Ashkenazi A.;
 RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
 RT colon cancer".
 RL Nature 396:699-703(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BLOOD;
 RX MEDLINE: 99253915.
 RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
 RT "A newly identified member of tumor necrosis factor receptor
 RT superfamily (TR6) suppresses LIGHT-mediated apoptosis".
 RL J. Biol. Chem. 274:13733-13736(1999).
 DR EMBL: AF104419; AAD03056.1; -
 DR EMBL: AF134240; AAD29688.1; -
 DR HSSP: P25942; ICDF
 DR INTERPRO: IPR000561; -
 DR INTERPRO: IPR001366; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS00186; EGF_2; UNKNOWN_1.
 DR PROSITE: PS00050; TNFR_NGFR_2; 2.
 KM Receptor.
 SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

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Query Match      19.3%; Score 433; DB 4; Length 300;
Best Local Similarity 42.9%; Pred. No. 2.6e-30;
Matches 69; Conservative 29; Mismatches 63; Indels 0; Gaps 0;

OY 5 PKYLYDETSHQLLCDKCPPTGYLKQHTAKWKTYCAPCPHHYDSDWHTSDECLYCSP 64
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 34 PLYPRMADATGRLVACACPPCTFYQRPORRSPPTTCGCPRRHYQGFNNYLERCHYCV 93
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 65 VKELQYVQKQECNRTNHNRYCECKEGRYLEIEFCLKHSRCPGPGVQVQACTPERNTYCKRC 124
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 94 LCGEEREERAFACHATHNRCRCRTGCFFAHAGCFLEHASCPCPAGVYAPGTPSQNTQCQPC 153
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 125 PDGFSENSSKAPCKRKHNCVFGLLTLQKGNATHDNICS 165
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 154 PGTFTSASSSSSECCOPHNCTALGLALNVPGSSSHDTLCT 194
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 7
OY PUS0 PRELIMINARY: PRT: 302 AA.
OY PUS0:
01-MAY-2000 (TREMBlrel. 13, Created)
01-MAY-2000 (TREMBlrel. 13, Last sequence update)
01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
NC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
[1]
RP SEQUENCE FROM N.A.:
RA Bobe J., Goetz F.W.:
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook
   trout (Salvelinus fontinalis) ovary at the completion of ovulation.";
RL Biol. Reprod. 0:0-0(1999).
DR EMBL; AF156738; AAD56428.1; -.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 302 AA; 34037 MM; E44C73477F05G3DF CRC64;

Query Match      18.1%; Score 405.5; DB 13; Length 302;
Best Local Similarity 45.2%; Pred. No. 6.6e-28;
Matches 71; Conservative 30; Mismatches 53; Indels 3; Gaps 2;

DB 11 DEETSHQLCDKCPPTGYLKQHTAKWKTYCAPCPDHYTDSWHTSDECLYCSPVCKELQ 70
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 27 DRYSLSTIYCDRCPPGTYLAPRASCAMRKSDCAECPNGATTEFNHNSKLCRS-MCAENQ 85
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 71 YKQSCNRTNHNRYCECKEGRYLEIEFCLKHSRCPGPGVQVQAGPENTYCKRNPDSF 128
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 86 VYKQSCSPNNGCECKEGRYLEIEFCLKHSRCPGPGVQVQAGPENTYCKRNPDSF 145
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 129 FSNSTSSKAPCKRKHNCVFGLLTLQKGNATHDNICS 165
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 146 YSEVSSAKATCLAGSNCKVGLRVYLKQGDWNTLCA 182
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 8
OY AC PRELIMINARY: PRT: 459 AA.
OY AC:
01-NOV-1996 (TREMBlrel. 01, Created)
01-NOV-1996 (TREMBlrel. 01, Last sequence update)
01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR 2 MRNA (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-NOD;
RX MEDLINE; 95178848.
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
   gene.";
RL Mann. Genome 5:726-727(1994).
DR EMBL; X76401; CAAS3981.1; -.
DR HSSP; P19438; INCF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
FT NON_TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MM; 6C51D2CF1C4626DF CRC64;

Query Match      15.4%; Score 345; DB 11; Length 459;
Best Local Similarity 25.2%; Pred. No. 2.2e-22;
Matches 100; Conservative 53; Mismatches 164; Indels 80; Gaps 12;

OY 9 HYDETSHQLLCDKCPPTGYLKQHTAKWKTYCAPCPHHYDSDWHTSDECLYCSPVCKE 68
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 31 YYDKRA-QMCCAKCPGQYVHFNCNKTSDTYCADCCEASMYQVANNQRTCLSCSSCST 88
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 89 LOYVQKQECNRTNHNRYCECKEGRYLEIEF-----CLKHSRCPGPGVQVQACTPERNTYCK 121
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 89 DQVETRACRQKQNRVACAEAGRYCALKTHSGRCRCMRLSKGPGFGVASSRAPNGNYLC 148
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 122 KRCPDGFSENSSKAPCKRKHNCVFGLLTLQKGNATHDNICGNSSTOKV-----174
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 149 KACAPGTTSDITSTSDVCPHRTCSILAI-----PGNASIDAVCAEESPLSLAIPRTLYVS 204
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 175 --DKHTGCP-----PCPAPPELL-----GAPSV-----ELFPPK 200
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 205 QPEPTRSQPLDQEPGSPQPTSLTSLGSPRIIEGSTKGISLPIGLIVGYSIGLMLGL 264
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 201 PKDTLMISRTPEVTCVVDVSHEDPEVKFNMYGVGEVYHNKTKRREDOYNSTRYVSVL 260
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 265 VNCFTLVORKKRPSCLQDA--KVPHVDEKSDAVGL-----EQQH-----LL 306
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 261 TYLHGDWNGKRYKKYKVNKALPA---PLEKTRISKAKQPREPOVYTLPPSNDLTKNQY 317
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 307 TTAPESSSSLESSASAGDRAPPGGHPOARVMAAQSQEARRASSRISDSSHGSHGTHV 366
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
OY 318 SLTCLVKGFPYPSDIWVESN-----GQPENNYKTP 349
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 367 NVTCLVNVCCSSDHSQCSQASATVGDPAKPSASP 403
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 9
OY AC PRELIMINARY: PRT: 439 AA.
OY AC:
01-NOV-1996 (TREMBlrel. 01, Created)
01-JAN-1999 (TREMBlrel. 09, Last sequence update)
01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91370690.
RA Dembic Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
   Brockhaus W., Leisauer W.;

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Db 54 YRHADRATGVLACDKCPACTYVSEHCTNTSLRYCSCSPVGTFRHENGIEKHCDSQPC 113
Qy 67 KEIQYKQECNKRHNRYCEKEGRHYIEFCLKHSRPPGCVYQACTPERNTYVCKPCPD 126
Db 114 PWDMEIKELPCALTDRECTRCPGFGFQSNATCAPRTVPCVWGVRKKTETEDVRCCKCAR 173
Qy 127 GFPSNERSASAPCRKHNGSVFGLLLFOKNATHDNICS---GNSESTQVYDKHTHPCPC 183
Db 174 GTSIDVPSSVMKCAVYDCLDSQNLVYIKPGIKETDNVCGTLPSFSSSTS----- 222
Qy 184 PABELLGPSEVFLPPPKRDTLMISRTPEYTCVYVDVSHED-----PEVKFNMYVDG 235
Db 223 PSP-----GTAIF---PRP-EHMEHVEPSSSTYVPGKMNSTESNSASVRRKV-LSSIQEG 273
Qy 236 VEYHNAKTRPREQOYNSTYVNVSVLVHODWLNKGEYCKKVSNAKLPADP---EKTIS 291
Db 274 TVPDNTSSSARGKEDVNT--LPNLQVYVNHQ---QGPHRHL--KLPSMEATGKERST 326
Qy 292 KAGGPR 298
Db 327 PIRPKR 333

RESULT 12
ID 090544 PRELIMINARY; PRT: 684 AA.
AC 090544;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DE 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE NOVEL ANTIGEN RECEPTOR PRECURSOR.
OS Ginglymostoma citratum (Nurse Shark).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Neoselachii; Galeomorphii; Galeoidea;
OC Orectolobiformes; Ginglymostomidae; Ginglymostoma.
[1]
RN SEQUENCE FROM N.A.
RP TISSUE-SPLEN;
RX MEDLINE: 95183140.
RA Greenberg A.S., Avila D., Hughes M., McKinney E.C.,
RA Flajnik M.F.;
RT "A new antigen receptor gene family that undergoes rearrangement and
RT extensive somatic diversification in sharks.";
RL Nature 374:168-173(1995).
EMBL: U18701; AAB48195.1; -.
DR INTERPRO: IPR003006; -.
DR PEAM: PF00047; 19; 6.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
DR SIGNAL.
RT CHAIN 1 18 POTENTIAL.
RT SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6DFD CRC64;
NOVEL ANTIGEN RECEPTOR.

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Db 459 SVSLKRP-PREELIWTQOTATVCEIY---YSDLENIKVFQWGVGERKKGVETQNDPMSG 514
Qy 252 STRVNVSVTLVHODWLNKGEYCKVSNKALPAPIEKTISKAK-GORPREQVYTLPPSRD 310
Db 515 SKSTIVSKLVMASEWDSGTEYVCLVEDSELPTPVKASIRKANVSQMHPRKYLHPSTD 574
Qy 311 EL-TKNQVSLTCLVKGYPYDIAVWESNGQ-PENNYKTTPLVDDSGFELYSKILTYDK 368
Db 575 EIDENSATIMLATNHPAEIYGVWANDTLDSGRTQVDSEKSGSSFEVDRLLTA 634
Qy 369 SRMOQGVFSCSVMHBALHN---HYTOKS 394
Db 635 AEMNSDTTYSCLVGHSPSLNDRILSTINKS 663

RESULT 13
ID 09060 PRELIMINARY; PRT: 384 AA.
AC 09060;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE SNC73 PROTEIN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
[1]
RN SEQUENCE FROM N.A.
RP Zheng S., Cao J., Cao W., Cai X., Geng L.;
RT "Identification and characterization of SNC73, a gene which is down-
RT regulated in colorectal cancer.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBU databases.
DR EMBL: AF067420; AAC19365.1; -.
DR INTERPRO: IPR003006; -.
DR PEAM: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
DR SEQUENCE 384 AA; 40947 MW; BAYADC3CA5A9DD48 CRC64;

Query Match 12.4%; Score 277.5; DB 4; Length 384;
Best Local Similarity 28.6%; Pred. No. 1.5e-16;
Matches 95; Conservative 35; Mismatches 141; Indels 61; Gaps 13;

Qy 115 PERNTYVCKRCPDGFSENE-----TSSKACRKHNGSVFGLLLTOR 155
Db 49 PDGQVVIACLVGFFPQEPPLSVTWSESGGVTAARNPPSQDAGDLXTTSSQLTPATO- 107
Qy 156 GNATHDNICGSESTQYDKTITCP-----PCPABELLGGSVFLFPKR----- 202
Db 108 -----CLAGKSVYCHV-KHYTNPSQDYVPCVPSTPPTPSTPST-PTPSPSCCHPR 157
Qy 203 -----DTLMSRTPEYTCVYVDVSHEDPEYKFMVYVDVGVHNAKTRPREQOYNSTY 254
Db 158 LSLHRALEDLLIGSEANLTCTLTG--RDASGVTFWTPTBSGR--SAVCGPRRDLCGY 214
Qy 255 RVVSVVLTVHODWLNKGEYCKVSNKALPAPIEKTISKAKGPREQVYTLPPSRDELTK 314
Db 215 SVSSVLPVPGCAEPNHNHKTFTCTAAYPESKPTLATLSKS-GNTFRREVHLLPPSEELAL 273
Qy 315 NO-VSLTCLVKGYPYDIAVWESNGQ--PENNYKTTPLVD-SDG--SFELYSKILTYDK 368
Db 274 NELVTLTCLARGFSPADVLRWLQGSQELPREKYLTVWASRQPSQGTTFVAVYSLRVAA 333
Qy 369 SRMOQGVFSCSVMHBALHNHYTOKSLSPG 400
Db 334 EDWKKGDTFCMVGHEALPLATQKTIIDRLAG 365

RESULT 14
ID 09Y606 PRELIMINARY; PRT: 616 AA.

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09Y606:
AC 01-NOV-1999 (Tremblrel. 12, Created)
DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF1A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 98032977.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- TISSUE SPECIFICITY: UNBIOLOGICAL EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AF018253; AAB86809.1; -
DR MIM; 603499; -
DR INTERPRO; IPR001368; -
DR PFM; PFO0020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 22
FT CHAIN 23 616
FT DOMAIN 24 212
FT TRANSSEM 213 233
FT DOMAIN 234 616
FT DOMAIN 33 195
FT REPEAT 33 69
FT REPEAT 70 112
FT REPEAT 113 152
FT REPEAT 153 195
FT DISULFID 34 46
FT DISULFID 47 60
FT DISULFID 50 68
FT DISULFID 71 86
FT DISULFID 92 112
FT DISULFID 114 124
FT DISULFID 126 133
FT DISULFID 127 151
FT DISULFID 154 169
FT DISULFID 175 194
FT CARBOHYD 105 105
FT CARBOHYD 174 174
SQ SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;
Query Match 11.5%; Score 258.5; DB 4; Length 616;
Best Local Similarity 34.5%; Pred. No. 1.2e-14;
Matches 58; Conservative 21; Mismatches 82; Indels 7; Gaps 4;

RESULT 15
ID 035305
AC 035305
DT 01-JAN-1998 (Tremblrel. 05, Created)
DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
INDUCED CYTOKINE RECEPTOR) (RANK).
GN TNFRSF1A OR RANK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE-LIVER EPITHELIUM;
RX MEDLINE; 98032977.
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tomelesko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
and dendritic-cell function.";
Nature 390:175-179(1997).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
DR EMBL; AF019046; AAB86810.1; -
DR HSSP; P25942; IGDF.
DR MGD; MGI:1314891; Tnfrsf11a.
DR INTERPRO; IPR000561; -
DR INTERPRO; IPR001368; -
DR PFM; PFO0020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1 30
FT CHAIN 31 625
FT DOMAIN 31 214
FT TRANSSEM 215 235
FT DOMAIN 236 625
FT DOMAIN 34 196
FT REPEAT 34 70
FT REPEAT 71 114
FT REPEAT 115 153
FT REPEAT 154 196
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 125
FT DISULFID 127 134
FT DISULFID 128 152
FT DISULFID 155 170
FT DISULFID 176 195
FT CARBOHYD 106 106
FT CARBOHYD 175 175
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E9951108E CRC64;
Query Match 11.5%; Score 256.5; DB 11; Length 625;
Best Local Similarity 25.3%; Pred. No. 1.8e-14;
Matches 102; Conservative 41; Mismatches 147; Indels 113; Gaps 17;

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OY 135 SKAPCRKHTNCVSFGLLTKGNATHDNICSGNSESTQKVDKTHTCPCPAPBLGSPV 194
Db 166 STDCKPMTNCTLLGKLEAHQGTESDVCGSSS-----MTLRPPKEAQYL--PSL 215
OY 195 FLPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNNYVGVHNAKTKPREQYNSTY 254
Db 216 IVL-----LFISSVVAAILIFGV-----YRKGR----- 241
OY 255 RVSVSLTVLHODWLN-----GKEY--KCRVSNKA-----LPAPIEKTIS 291
Db 242 ----ALTANLMNWNVDACSSLSGKNKSSGDRCAGSHSATSSQOVCBGILLMTREKMP 297
OY 292 K-----AKGP-----REPOVTL-----PSRDELT--KNQVSLTCL 322
Db 298 EDGAGVCGPVCAGGPAEYRDSRTFTLVSEVETQGDLSRKIPTEDYTDPSOPSTGSL 357
OY 323 V-----KGFYPSDIAVEMESNGOPENNYKTPPVLDSDGSFF 359
Db 358 LLIQGSKSIRPFQEPLEVGENDLSOCFTGTSTYDSECDF 400

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Search completed: December 27, 2000, 10:52:40
 Job time: 71 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:29 ; Search time 60.82 Seconds
(without alignments)
615.637 Million cell updates/sec

Title: US-09-389-545-2
Perfect score: 2179
Sequence: 1 MNKKLCCALVLDLIEWT.....OKLFLEMIGNOVSKISCL 401

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Number of hits satisfying chosen parameters: 297973

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database :
1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MHC:*
8: SP_ORGANELLE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	11 008712	008712 mus musculu
2	2079	95.4	401	11 008727	008727 rattus norv
3	1892	86.8	401	4 000300	000300 homo sapien
4	1789	82.1	372	4 090404	090404 homo sapien
5	424.5	19.5	300	4 095407	095407 homo sapien
6	390.5	17.9	302	13 09PUS0	09PUS0 salvelinus
7	314	14.4	459	11 063327	063327 mus musculu
8	302.5	13.9	482	11 008734	008734 mus musculu
9	301.5	13.8	655	4 075309	075309 homo sapien
10	298	13.7	439	4 016042	016042 mus musculu
11	268.5	12.3	625	11 035305	035305 mus musculu
12	266.5	12.2	616	4 09Y806	09Y806 homo sapien
13	226	10.4	355	12 085308	085308 compox viru
14	224	10.3	349	12 057098	057098 camelpon vi
15	222.5	10.2	349	12 057305	057305 compox viru
16	220	10.1	349	12 057284	057284 camelpon vi
17	220	10.1	349	12 057097	057097 camelpon vi
18	219	10.1	349	12 057110	057110 variola vir
19	218	10.0	349	12 057111	057111 variola vir

ALIGNMENTS

RESULT	1	ALIGNMENTS
008712	PRELIMINARY:	PRT: 401 AA.
AC 008712:	O70202:	
DT 01-JUL-1997 (TREMBLrel. 04, Created)		
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)		
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)		
DE OSTEOCYTE-PECursor (OSTEOCYTOGENESIS INHIBITORY FACTOR)		
DE (OCIF).		
GN TNFRSF11B OR OPG.		
OS Mus musculus (Mouse).		
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;		
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
RN [1]		
RC SEQUENCE FROM N.A.		
RP STRAIN=BAIB/C; TISSUE=KIDNEY;		
RX MEDLINE: 97262071.		
RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,		
RA Luethy R., Nguyen H.O., Wooden S., Bennett L., Boone T., Shimamoto G.,		
RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,		
RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,		
RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,		
RA Suggs S., Boyle W.J.,		
RT "Osteoprotegerin: a novel secreted protein involved in the regulation		
RT of bone density.";		
RL Cell 89:309-319(1997).		
RN [2]		
RC SEQUENCE FROM N.A.		
RP STRAIN=129/OLA, AND NIH SWISS;		
RX MEDLINE: 98382527.		
RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,		
RA Higashio K.;		
RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)		
RT gene and its expression in embryogenesis.";		
RL Gene 215:339-343(1998).		
CC - FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES		
CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY		
CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO		
CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN		
CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.		
CC - SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).		
CC - SUBCELLULAR LOCATION: EXTRACELLULAR.		

CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94331; AAB53708.1; -.
 DR EMBL: AB013898; BAA28269.1; -.
 DR EMBL: AB013903; BAA33388.1; -.
 DR EMBL: AB013899; BAA33388.1; JOINED.
 DR EMBL: AB013900; BAA33388.1; JOINED.
 DR EMBL: AB013901; BAA33388.1; JOINED.
 DR EMBL: AB013902; BAA33388.1; JOINED.
 DR HSSP: P25942; ICDP.
 DR MGD: MG1:109587; OP9.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS30017; DEATH_DOMAIN; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR Glycoprotein: Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
 FT SEQUENCE 401 AA; 45923 MW; CAA6102D3B12470 CRC64;
 Query Match 100.0%; Score 2179; DB 11; Length 401;
 Best Local Similarity 100.0%; Pred. No. 2.5e-165;
 Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 181 HDNVCSGNREATOKGIDVTLCGEAFRRFAVPTKIIIPNMLSVLYDSLPGTVNAESVERI 240
 QY 241 KRHSSEQFQFLKLKHKHNRQDEMYKKIIODIDCESSVQRIHGSNTTOLLAME 300
 Db 241 KRHSSEQFQFLKLKHKHNRQDEMYKKIIODIDCESSVQRIHGSNTTOLLAME 300
 QY 301 SLPGKKSPEIERETRTCKSSBOLKLSLMLRKINGDOQTLLGLMALKLTSHPPT 360
 Db 301 SLPGKKSPEIERETRTCKSSBOLKLSLMLRKINGDOQTLLGLMALKLTSHPPT 360
 QY 361 VTHSLRTMRFLSHFTMYRLYQKLFLEMIGNOVQSVKISCL 401
 Db 361 VTHSLRTMRFLSHFTMYRLYQKLFLEMIGNOVQSVKISCL 401
 RESULT 2
 ID 008727 PRELIMINARY; PRT; 401 AA.
 AC 008727;
 DT 01-JUN-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSP1B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE: 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehly R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trall G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density.";
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: U94330; AAB53707.1; -.
 DR HSSP: P25942; ICDP.
 DR INTERPRO: IPR001368; -.
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KM Glycoprotein: Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 201 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.

FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 SQ SEQUENCE 401 AA; 46192 MW; EEC6A31F1D4E573A CRC64;

Query Match 95.48; Score 2079; DB 11; Length 401;
 Best Local Similarity 94.56; Pred. No. 2.2e-157;
 Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;

QY 1 MNKMLCCALLVLDLIIEMTTOETLPKYLHYDPETGHOGLCDKCAPGYLKHQCHTVRRKT 60
 DB 1 MNKMLCCALLVLDLIIEMTTOETLPKYLHYDPETGHOGLCDKCAPGYLKHQCHTVRRKT 60
 QY 61 LCVPCPDHSTYDSWHTSDCVYCSVPCKELQSVKQECNTHRVCECEGRYLEIEFCLK 120
 DB 61 LCVPCPDHSTYDSWHTSDCVYCSVPCKELQSVKQECNTHRVCECEGRYLEIEFCLK 120
 QY 121 HRSCPPGSGVAGTSPRNTVCKKCPDGFSGSETSSKAPCKKHNCSTFGILLIOKGNAT 180
 DB 121 HRSCPPGSGVAGTSPRNTVCKKCPDGFSGSETSSKAPCKKHNCSTFGILLIOKGNAT 180
 QY 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKILPMWLSLVDSLPCTVNAESVERI 240
 DB 181 HDNVCSGNREATQKCGIDVTLCCEAFRFAVPTKILPMWLSLVDSLPCTVNAESVERI 240
 QY 241 KRRHSSQEQTFQLIKLNKHONRQDMVKKIIQDIDLCSSVQRLGHSNLTTEQLALME 300
 DB 241 KRRHSSQEQTFQLIKLNKHONRQDMVKKIIQDIDLCSSVQRLGHSNLTTEQLALME 300
 QY 301 SLPEKRTISPEIERTKRTCKSSBOLLKLSIMRKNGDDOPLKLMALKLTKTSHEPKT 360
 DB 301 SLPEKRTISPEIERTKRTCKSSBOLLKLSIMRKNGDDOPLKLMALKLTKTSHEPKT 360
 QY 361 VTHSLKRTMRFLSHFTMYRLYQKLFLEMIGNOVQSVKISCL 401
 DB 361 VTHSLKRTMRFLSHFTMYRLYQKLFLEMIGNOVQSVKISCL 401

RESULT 3

000300 PRELIMINARY; PRT; 401 AA.

AC 000300: 060236;
 DT 01-JUL-1997 (Tremblrel. 04, Created)
 DT 01-JUL-1997 (Tremblrel. 04, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11b).
 GN TNRSEFLIB OR OPG OR OCIF.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-KIDNEY;
 RC MEDLINE: 97262071.
 RA Stimonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Laetey R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.,
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 of bone density.";
 RT Cell 89:309-319(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LUNG FIBROBLAST;
 RC MEDLINE: 98151033.
 RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N.,
 RA Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A.,
 RA Tada E., Morinaga T., Higashio K.;
 RT "Identity of osteoclastogenesis inhibitory factor (OCIF) and

RT osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits
 RT osteoclastogenesis in vitro.";
 RL Endocrinology 139:1329-1337(1998).
 RN [3]

RP SEQUENCE FROM N.A.
 RC TISSUE-PLACENTA;
 RC MEDLINE: 98351569.
 RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;
 RT "Cloning and characterization of the gene encoding human
 RT osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Eur. J. Biochem. 254:685-691(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART,
 CC KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN
 CC A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN
 CC THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB008822; BAA32076.1; -.
 DR EMBL: AB008821; BAA32076.1; JOINED.
 DR EMBL: U94332; AAB53709.1; -.
 DR HSSP: P25942; ICDF.
 DR MIM: 602543; -.
 DR INTERPRO: IPR001368; -.
 DR PRAM: P700020; TNFR_c6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 183
 FT REPEAT 23 63
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 63 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 98
 FT CARBOHYD 152 152
 FT CARBOHYD 165 165
 FT CARBOHYD 178 178
 FT CARBOHYD 289 289
 FT CONFLICT 263 263
 SQ SEQUENCE 401 AA; 45996 MW; EB42FA51C9D7C71E CRC64;
 A -> D (IN REF. 2 AND 3).

Query Match 86.88; Score 1892; DB 4; Length 401;
 Best Local Similarity 85.68; Pred. No. 1.5e-142;
 Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

QY 1 MNKMLCCALLVLDLIIEMTTOETLPKYLHYDPETGHOGLCDKCAPGYLKHQCHTVRRK 59
 DB 1 MNKMLCCA-LVFLDISIKMTQETFPKYLHYDEBESHOLCDKCAPGYLKHQCHTAKK 59
 QY 60 TLVPCPDHSTYDSWHTSDCVYCSVPCKELQSVKQECNTHRVCECEGRYLEIEFCL 119
 DB 60 TVLAPCPDHYTDSWHTSDCLYCSVPCKELQYVKECNTNRHVCECEGRYLEIEFCL 119
 QY 120 KHSCPPGSGVAGTSPRNTVCKKCPDGFSGSETSSKAPCKKHNCSTFGILLIOKGN 179
 DB 120 KHSCPPGSGVAGTSPRNTVCKKCPDGFSGSETSSKAPCKKHNCSTFGILLIOKGN 179

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Db 120 KHRSCPPGFGVQAQTPERNVYCKRCPCDGFSENETSSKAPCKKHTNCSVFGLLTKQKNA 179
Qy 180 THDNVCSGNREATQKCGIDVTLCCEAFERFAVPKTIIPNWLVSVDLPGTKVNAESVER 239
Db 180 THDNICSGNSESTQKCGIDVTLCCEAFERFAVPKTFPMNLVSVDNPGTKVNAESVER 239
Qy 240 IKRRHSSQEQFQOLKIMKHONRQDEMVKTIHODIDLCSSVORHSHNLTTEQLALM 299
Db 240 IKRQSSQEQFQOLKIMKHONKADIVKTIHODIDLCNSVORHSHNLTTEQLALM 299
Qy 300 ESLPKKISPEEIERTRKCKSSQOLKLSLMRKNGDQDTLKGIMLYALKHLKTSHPFK 359
Db 300 ESLPKKISPEEIERTRKCKSSQOLKLSLMRKNGDQDTLKGIMLYALKHLKTSHPFK 359
Qy 360 TVTSHLRKTMFLSHPTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 360 TVTOSLKTIRFLSHPTMYRLYOKLFLEMIGNOVOSVKISCL 401

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RESULT 4
Q9UHP4 PRELIMINARY; PRT; 372 AA.
09UHP4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE OSTEOPOTEGERIN (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PLACENTA.
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
DR EMBL; AF134187; AAF20168.1; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF000020; TNFR_C6; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
FT NON-TER
SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

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Query Match 82.1%; Score 1789; DB 4; Length 372;
Best Local Similarity 86.0%; Pred. No. 2,1e-134;
Matches 320; Conservative 25; Mismatches 27; Indels 0; Gaps 0;

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22 EULPKYLYHDEPETHQOLCDKCAPGYLYKQCTYRKTLVPCPDHSTYDSMHTSDECV 81
1 EFPFKYLYHDEPETHQOLCDKCPGTLYKQCTAKMKYVCAPCPDHYTSDMHTSDECV 60
Qy 82 YCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTERNTV 141
Db 61 YCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTERNTV 120
Qy 142 CKKCDGFFSGSTSKAPKIKTNGSTFGLLLIOKGNATHDNCVSNRATOKCGIDVT 201
Db 121 CKRCDGFFSGSTSKAPKIKTNGSTFGLLLIOKGNATHDNCVSNRATOKCGIDVT 180
Qy 202 CEAFERFAVPKTIIPNWLVSVDLPGTKVNAESVERIKRRHSSQEQFQOLKIMKHON 261
Db 181 CEAFERFAVPKTIIPNWLVSVDLPGTKVNAESVERIKRRHSSQEQFQOLKIMKHON 240
Qy 262 RDOEWVKKIIQDIDLCSSVORHSHNLTTEQLALMSESLPGKISPEEIERTRKCKS 321
Db 241 KQDYLKTIQDIDLCNSVORHSHNLTTEQLALMSESLPGKISPEEIERTRKCKS 300
Qy 322 SEQLLKLSLMRKNGDQDTLKGIMLYALKHLKTSHPKTVTSHLRKTMFLSHPTMYRLY 381
Db 301 SPOILKLSLMRKNGDQDTLKGIMLYALKHLKTSHPKTVTSHLRKTMFLSHPTMYRLY 360

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Qy 382 OKLFLEMIGNOV 393
Db 361 OKLFLEMIGNOV 372

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RESULT 5

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Q95407 PRELIMINARY; PRT; 300 AA.
AC 095407;
ID 095407;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE DECOY RECEPTOR 3.
GN DC33 OR TR6.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 99087326.
RA Pictl R.M., Maisters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.B., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RL colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE; 99253915.
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
DR EMBL; AF104419; AAD03056.1; -.
DR EMBL; AF134240; AAD29688.1; -.
DR HSSP; P25942; ICDF.
DR INTERPRO; IPR000561; -.
DR INTERPRO; IPR001368; -.
DR PFAM; PF000020; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
KW Receptor
SQ SEQUENCE 300 AA; 32679 MW; F90AEE33718449AF CRC64;

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Query Match 19.5%; Score 424.5; DB 4; Length 300;
Best Local Similarity 39.0%; Pred. No. 3,2e-26;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;

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Qy 26 PKYLYHDEPETHQOLCDKCAPGYLYKQCTYRKTLVPCPDHSTYDSMHTSDECVYCS 85
Db 34 PLYWRDAEETGRILVCAQCPGTFOVORCDRSDPTTCGCPRHDTORWNLERCRCNV 93
Qy 86 VKELQSVKQECNRTNHNVCCEEGRYLEIEFCLKHSRCPGSGVVOAGTERNTVCKK 145
Db 94 LCGEREERARCAHATNNAACRKTGFENHAGFCLEHASCPPGAGVIATGATISQNTQCP 153
Qy 146 PDGFSGFTSSKAPKIKTNGSTFGLLLIOKGNATHDNCVSNRATOKCGIDVTLC 202
Db 134 PPGTSSASSSSQCPHRCNTAIGLALNVAAGSSSHDILCTSCIGFPLSTVPAEAE--C 211
Qy 203 EEAERFAVPKTIIPNWLVSVDL 227
Db 212 ERAVIDFAFDISIKRLQRLQL 236

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RESULT 6
Q9PUS0 PRELIMINARY; PRT; 302 AA.
ID 09PUS0
AC 09PUS0;

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QY . 156 SKAPCIKHTNCST

Db 184 STDVCRPHRIS----LAIKGNASTDAVCA 210

RESULT 9

075509 PRELIMINARY; PRT; 655 AA.
 AC 075509;
 DT 01-NOV-1998 (TREMblrel. 08, Created)
 DT 01-NOV-1998 (TREMblrel. 08, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE TNFR-RELATED DEATH RECEPTOR-6.
 DR6.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pan G., Bauer J.H., Haridas V., Wang S., Liu D., Ni J., Yu G.,
 RA Vincenz C., Aggarwal B.B., Dixit V.M.;
 P "Identification and functional characterization of DR6, a novel death
 domain-containing TNF receptor."
 Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF068868; AAC34583.1; -.
 DR INTERPRO: IPR000488; -.
 DR INTERPRO: IPR001368; -.
 DR PRAM; PF000020; TNFR_c6; 4.
 DR PRAM; PF00531; death; 1.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS50017; DEATH_DOMAIN; 1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 SO SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;

Query Match 13.8%; Score 301.5; DB 4; Length 655;

Best Local Similarity 29.0%; Pred. No. 4,7e-16;

Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

QY 10 LVLDIIEMTQ-----TLPKYLHDPETGHLDDCKAPGYLKHQCTVRRKTLICV 63
 Db 30 LLLGLSTTTAOPBOKASNLIGTRHVDRAVGOLTDCKPAGYVSEHSTSLRCS 89
 QY 64 PCPDHSDYDNTSECVYCSPVCKELQSVKQECNRTNHRVCECEGRYLEIEFCLKHRS 123
 Db 90 SCPTGTFTRHNGIEFKCHDCQPCPWPMEIKLPCALDRECTCPGAFQSNATCAPITV 149
 QY 124 CPSSGVVQACTPERNTVCKCPDFFSGEISSKAPCIKHTNCTFGILLIQGNATHDN 183
 Db 150 CPVGMGVKAKGTETEDVRCOCARGTFSVSVKCKRAYTDCLSQNLVLIKPTKETDN 209
 Db 184 VC-----SGNRATQKCGIDVYLCEAFRFAVPMK-IIPNLSVYVDSLPGTKVAESVE 238
 Db 210 VCGTLPSSSTSPGAIAPRPHMETHEVPSSTYVPKGN-----STSSNASV 262
 QY 239 RIKRRHSSQEQFOLLKMKHQN-----RDQEMVKKIIDIIDLCSSVORHLGHSNLTQEQ 294
 Db 263 RPKVLSSTQETVP-----DNTSSAKGKEDVKTLPNLQVNVHQGPHRH-----ILK 311
 QY 295 LLAIMESLPGKKIS 308
 Db 312 LIPMEATGEGKSS 325

RESULT 10
 ID 016042 PRELIMINARY; PRT; 439 AA.
 AC 016042;
 DT 01-NOV-1996 (TREMblrel. 01, Created)
 DT 01-JAN-1999 (TREMblrel. 09, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 91370690.
 RA Dembicz Z., Loetscher H., Gubler U., Pan Y.C., Lahm H.W., Gentz R.,
 RA Brockhaus M., Lesslauer W.;
 RT "Two human TNF receptors have similar extracellular, but distinct
 RT intracellular, domain sequences."
 RL Cytokine 2:231-237(1990).
 DR EMBL; S63368; AAB19824.1; -.
 DR HSSP; P25942; ICDF.
 DR INTERPRO: IPR001368; -.
 DR PRAM; PF000020; TNFR_c6; 4.
 DR PROSITE; PS00652; TNFR_NGFR_1; 2.
 DR PROSITE; PS50050; TNFR_NGFR_2; 3.
 SO SEQUENCE 439 AA; 46090 MW; FEBCBEB329CC67FF6 CRC64;

Query Match 13.7%; Score 298; DB 4; Length 439;

Best Local Similarity 35.6%; Pred. No. 5,5e-16;

Matches 62; Conservative 15; Mismatches 75; Indels 22; Gaps 3;

QY 31 YDPETGH-----QLLDCAPGYLKHQCTVRRKTLICVPCPDHSDYDNTSD 78
 Db 10 YAPPGSTCRLEYRDDTAQWCCSCSPGOHAKVCTKTSIDTCDSCEDSTYQILMMVP 69
 QY 79 ECYVCSVPCKELQSVKQECNRTNHRVCECEGRYLE-----EFCLKHSCPGSGVQ 132
 Db 70 ECLSGSRCSDDVETACTEONRITCRPGWICALSKQBGCHLAPLKCRBGFVAR 129
 QY 133 AGTEPRNTVCKCPDFFSGEISSKAPCIKHTNCTFGILLIQGNATHDNVCS 186
 Db 130 PGTEISDVYCKPCAPGFSNMTSTSDICRPHQICNVVAI-----PGNSMAYVCT 179

RESULT 11

035305 PRELIMINARY; PRT; 625 AA.

AC 035305;
 DT 01-JAN-1998 (TREMblrel. 05, Created)
 DT 01-JAN-1998 (TREMblrel. 05, Last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 DE INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF1A OR RANK
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-LIVER EPITHELIUM;
 RX MEDLINE; 98032977.
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function."
 RL Nature 380:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL; AF019046; AAB86810.1; -.
 DR HSSP; P25942; ICDF.
 DR MGD; MGI:1314891; Tnfrsf1a.
 DR INTERPRO: IPR000561; -.
 DR INTERPRO: IPR001368; -.
 DR PRAM; PF000020; TNFR_c6; 3.
 DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE; PS01186; EGF_2; UNKNOWN_1.
 DR PROSITE; PS50050; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1
 FT CHAIN 31 625 RECEPTOR ACTIVATOR OF NF-KAPPA-B.

FT DOMAIN 31 214 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 215 235 POTENTIAL.
 FT DOMAIN 236 625 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 34 196 4 X TNFR-CYS.
 FT REPEAT 34 70 TNFR-CYS 1.
 FT REPEAT 71 114 TNFR-CYS 2.
 FT REPEAT 115 153 TNFR-CYS 3.
 FT REPEAT 154 196 TNFR-CYS 4.
 FT DISULFID 35 47 BY SIMILARITY.
 FT DISULFID 48 61 BY SIMILARITY.
 FT DISULFID 51 69 BY SIMILARITY.
 FT DISULFID 72 87 BY SIMILARITY.
 FT DISULFID 93 113 BY SIMILARITY.
 FT DISULFID 115 125 BY SIMILARITY.
 FT DISULFID 127 134 BY SIMILARITY.
 FT DISULFID 128 152 BY SIMILARITY.
 FT DISULFID 155 170 BY SIMILARITY.
 FT DISULFID 176 195 BY SIMILARITY.
 FT CARBOHYD 106 106 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 175 175 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 625 AA; 66621 MW; F8C1872E951D8E CRC64;

Query Match 12.3%; Score 268.5; DB 11; Length 625;
 Best Local Similarity 29.9%; Pred. No. 1.8e-13;
 Matches 88; Conservative 34; Mismatches 123; Indels 49; Gaps 14;

QY 7 CALLVLDIIEMTQETLP--KYLHYPETGQLDCKAPGYTLKQHCVRKRLTCLVP 64
 DB 19 CVLLVPLQV---TLQVTPCTQERHYE-HLGR--CCSRCEPGLYSKCTPTSDSVCLP 71
 QY 65 CPHSTSDSHNTSDCYVCSYVC--KELOSAYQECRTNRRVCECEGRV--LEIEFCL 119
 DB 72 CGPDEYLDSTNEDKCL-LHKVCDAGALVAV-DPGNHTAPRCACAGYHMSDCCCR 129
 QY 120 KHRSCPPGSGVYAGTPEKNTVCKCPDFFSGETSSKAPCIKHTNCTGFLLIQKNA 179
 DB 130 RNECAPRGFAQHPLQNKDTVCTPCLGFSDFVSSTDKCRKWTNCTLGKLEAHGTT 189
 QY 180 THNVCSGN-----REATQKCGIDVTLCENAFREAVPTKII----- 216
 DB 190 ESDVVCSSSTLRPRPKQAVYPLSLVL--LFISVYVAALIFGVYKRGKALTANL 247
 QY 217 PMLSLVLSVLPSTKYNASVERIKRRH---SSQEQFOLKMLKHNROENV 267
 DB 248 WNVNWDACSSLGSK--ESSGDRACGSHATSSQOVCBGLL--MTREKRV 296
 RESULT 12
 ID 09Y606 PRELIMINARY; PRT: 616 AA.
 AC 09Y606;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF1A OR RANK.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 96032977.
 RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougal W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Galibert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 and dendritic-cell function."
 RT Nature 390:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: UBIQUITOUS EXPRESSION WITH HIGH LEVELS IN

CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
 CC GLAND.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: AF018253; BAB86809.1; .
 CC MIM: 603499; .
 DR INTERPRO: IPR001368; .
 DR PIRAM: P00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS0050; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1 22
 FT DOMAIN 23 616
 FT TRANSMEM 215 233
 FT DOMAIN 234 616
 FT DOMAIN 33 195 4 X TNFR-CYS.
 FT REPEAT 33 69 TNFR-CYS 1.
 FT REPEAT 70 112 TNFR-CYS 2.
 FT REPEAT 113 152 TNFR-CYS 3.
 FT REPEAT 133 195 TNFR-CYS 4.
 FT DISULFID 34 46 BY SIMILARITY.
 FT DISULFID 47 60 BY SIMILARITY.
 FT DISULFID 50 68 BY SIMILARITY.
 FT DISULFID 71 86 BY SIMILARITY.
 FT DISULFID 92 112 BY SIMILARITY.
 FT DISULFID 114 124 BY SIMILARITY.
 FT DISULFID 126 133 BY SIMILARITY.
 FT DISULFID 127 151 BY SIMILARITY.
 FT DISULFID 154 169 BY SIMILARITY.
 FT DISULFID 175 194 BY SIMILARITY.
 FT CARBOHYD 105 105 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 174 174 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 616 AA; 66033 MW; E3DE9A/A08196F81 CRC64;

Query Match 12.2%; Score 266.5; DB 4; Length 616;
 Best Local Similarity 24.4%; Pred. No. 1.2e-13;
 Matches 108; Conservative 54; Mismatches 166; Indels 115; Gaps 21;

QY 5 LCCALLVLDIIEMTQETLP--KYLHYPETGQLDCKAPGYTLKQHCVRKRLTCL 62
 DB 16 LCCALLVLDIIEMTQETLP--KYLHYPETGQLDCKAPGYTLKQHCVRKRLTCL 62
 QY 63 VPCPDSTSDSHNTSDCYVCSYVC--KELOSAYQECRTNRRVCECEGRV--LEIEF 117
 DB 69 LPCGPDEYLDSTNEDKCL-LHKVCDTGAALVAVAG-NSTTPRCACAGYHMSDCC 126
 QY 118 CLKHRSCPPGSGVYAGTPEKNTVCKCPDFFSGETSSKAPCIKHTNCTGFLLIQK 177
 DB 127 GRNTECAPRGFAQHPLQNKDTVCTPCLAGFSDFVSSTDKCRKWTNCTLGKLEA 186
 QY 178 NATHNVCSGNREATQKCGIDVTLCENAFREAVPTKII----- 216
 DB 187 TEKSDAVCSSLPARKPNEPHYLLPGLIIL--LFASVALVAALIFGVYKRGKALT 243
 QY 217 ---PMLSLVLSVLPSTKYNASVERIKRRHS-----QEQFOLKML 257
 DB 244 ANLWMINACGRLSGDK--ESSGDSVSTHANGQACGCVLLLTLEETFEPMCY 301
 QY 258 KH-----ONRQEWKRIIDIDICESSVOR-----HIGSNLTLEOL 295
 DB 302 PDQGVYCOGTGVGGPYAGGEDARML-SLVSKTEIEDSFROMPDEYMDRPSQPTOL 360
 QY 296 LALMESLPGRKISPP--EEIE-----RTKRT-----CKSSQOLKLLSLMR 335
 DB 361 LFLTE--PSKSPSPSEPLEVGENDSLQCTGTGSSSCNCTEPLCR----- 411
 QY 336 NGDQDLKGLMALKLTKTSHP 358
 DB 412 --DWTMSSSENLYQKREVDGHC 432
 RESULT 13

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085308
ID 085308 PRELIMINARY; PRT: 355 AA.
AC 085308;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE SECRETED RECEPTOR BINDING TUMOR NECROSIS FACTOR (CRMB).
GN CRMB.
OS Cowpox virus (CPV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED.
RC MEDLINE; 83117629.
RA Pickup D.J., Bastia D., Stone H.O., Joklik W.K.;
RT "Sequence of terminal regions of cowpox virus DNA: arrangement of
RT repeated and unique sequence elements."
RL Proc. Natl. Acad. Sci. U.S.A. 79:7112-7116(1982).
RN [2]
SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED.
RC MEDLINE; 90177240.
RA Parsons B.L., Pickup D.J.;
RT "Transcription of orthopoxvirus telomeres at late times during
RT infection."
RL Virology 173:69-80(1990).
RN [3]
SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED.
RC MEDLINE; 91196263.
RA Hu F.O., Pickup D.J.;
RT "Transcription of the terminal loop region of vaccinia virus DNA 1s
RT initiated from the telomere sequences directing DNA resolution."
RL Virology 181:716-720(1991).
RN [4]
SEQUENCE FROM N.A.
RP STRAIN-BRIGHTON RED.
RC MEDLINE; 94378510.
RA Hu F.O., Smith C.A., Pickup D.J.;
RT "Complex virus contains two copies of an early gene encoding a soluble
RT secreted form of the type II TNF receptor."
RL Virology 204:343-356(1994).
DR EMBL; L08906; AAA60952.1; -.
DR HSP; P19438; 1TNR.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
DR SEQUENCE 355 AA; 39008 MW; 2C9E5C0D42FA4B3 CRC64;
Query Match 10.4%; Score 226; DB 12; Length 355;
Best Local Similarity 24.1%; Pred. No. 2.2e-10;
Matches 85; Conservative 49; Mismatches 141; Indels 78; Gaps 15;
QY 9 LVLVDDITETQETLPRKYLHPDEG-----HQLCDKCAPTYLKHQC--IVR 57
DB 6 LLLLSCTIITNSDTP-----HEPSNGCKDNEYKRHHLLCCLSCPPTVYASRLCDSTKN 60
QY 58 RKTLCVPCPDHSYTDSWHTSDECVYCSVPCKELOSVKOECKRTHNRVCECEGRYLEI-- 115
DB 61 TMTCTPASPFTFSRNHHLRACLSGCRDSNOVETRSCTTHNRITDCAPGYICFLKG 120
QY 116 ----EFCLEKHSRCPGSGVQAGTPERTNVCCKCPDGFSEGTSSKAPCIKHTNCSFGL 171
DB 121 SSGCKACVSGTCKGIGYV--VSGHTPTGTVCSPCGLGYSHVSSVDC--EPVPSNTENY 178
QY 172 LLIQKG-NATHDNYC-----SGNRATOKGIDVTL-----CEAFAFRVAVPTKIIPNMLS 221
DB 179 IDEELNLPVNDTSCTRTTGTGLESISTSELITIMNKKDDPVERN-----GYFS 229
QY 222 VLVDSLPG-----TKV---NAESVERIKRHSSEQGTQLLKKHQRDDEM 266

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DB 230 VLVNVAASGFTGONRQYNSKVTCTLNEFIKCNKNSYSSSKQ-----LTKRKNDDSI 283
QY 267 V--KKIIDIIDLCESSVQRHLGHSNLTE-----QLALMESIPGK 305
DB 284 MPHESTVLVGDCLSSVDIYILXSNMTQYEMDTISYHGAVLVDVDSHMPGR 336
RESULT 14
ID 057098 PRELIMINARY; PRT: 349 AA.
AC 057098;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Camelox virus (strain CP-1).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
[1]
RN SEQUENCE FROM N.A.
RP STRAIN-SAUDI-M3.
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RL EMBL; U87839; AAB94356.1; -.
DR HSP; P25942; 1CDF.
DR INTERPRO; IPR001368; -.
DR PFAM; PF00020; TNFR_C6; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR SEQUENCE 349 AA; 37978 MW; 8630EFAED7A584B5 CRC64;
Query Match 10.3%; Score 224; DB 12; Length 349;
Best Local Similarity 24.9%; Pred. No. 3.2e-10;
Matches 76; Conservative 41; Mismatches 126; Indels 62; Gaps 13;
QY 31 YDEPTG-----HQLCDKCAPTYLKHQCIVRRKKTLCVCPDHSYTDSWHTSDECV 81
DB 25 YAPNSGCKDNEYKRHHLLCCLSCPPTVYASRLCDSTKNTQCTPGSGTFSRNHHLRAC 84
QY 82 YCSVPCKELOSVKOECKRTHNRVCECEGRYLEI-----EFCLEKHSRCPGSGVQAGT 135
DB 85 SCNRCDSONVETRSCTTHNRICECSPGYICILKSSGCKACVSGTCKGIGYV--VSGHT 143
QY 136 PERFTVCKKCPDGFSEGTSSKAPCIKHTNCSFGLLIQKG-NATHDNYC-----SGNR 189
DB 144 SAGDVICSPGCLGYSTRVGSADKC--EPVPSNTENYIDEVLNLPVNDTSCTRTTGTGIS 202
QY 190 EATOKGIDVTL-----CEAFAFR--FAVPTKIIPNMLSVLVDSLPGKRVNAESVERIKR- 242
DB 203 ESISTSELITIMNKKDDPVEREYFSVLNV-----ATSGFTTANRQYNSKY 252
QY 243 -----RHSSQGTQLLKKHQRDDEMVKKIIDIIDL--CESSVQRHLGHS 288
DB 253 CTLNEFIKCNKNSYSSSKQ-----LTKRKNDGIMPS--ETVTLAGDCLSSVDIYILS 304
QY 289 NLTE 293
DB 305 NTNTQ 309
RESULT 15
ID 057305 PRELIMINARY; PRT: 349 AA.
AC 057305;
DT 01-JUN-1998 (Tremblrel. 06, Created)
DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
DE TUMOR NECROSIS FACTOR RECEPTOR II HOMOLOG.
GN CRMB.
OS Cowpox virus (CPV).

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OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MUNICH OPV89/5(CAT), MUNICH OPV 91/1(CAT);
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: U90233; AAB94389.1; -;
DR EMBL: U90228; AAB94384.1; -;
DR HSSP: P19438; ITNR.
DR INTERPRO: IPR001368; -;
DR PFAM: PF00020; TNFR_C6; 2.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_2.
DR PROSITE: PS50050; TNFR_NGFR_2; 1.
SQ SEQUENCE 349 AA; 38063 MW; 424EE08FDEDD04CF CRC64;

Query Match 10.2%; Score 222.5; DB 12; Length 349;
Best Local Similarity 25.6%; Pred. No. 4, 2e-10;
Matches 81; Conservative 47; Mismatches 144; Indels 45; Gaps 14;
QY 9 LVLVDIIEMTQETLPKYLHPETG-----HQLCDKCAPGYLKQHC--TYR 57
DB 6 LLLLLSCIIILINSIDTP----HEPSNGKCKDNEYRHHLCCLSCPPTYASRLCDSTN 60
QY 58 RKLVCPCPDHSTYDSDMHTSDECVYCSPVCKELQSVKQECNRTNHRNCECEGRYLEI-- 115
DB 61 TMTQCTPCSGSGFTSRNNHLPACLSCNGRCDSNQVKTNRSCNTTHNRICDCAFGYCLLG 120
QY 116 ---EFCLKHRSCPPSGVVOAGTPERNVTVCCKCPDGFSGETSSKAPCIKHTNCSTFGL 171
DB 121 SSGCKACVSGOTKCGIGY-GVSGHTPTGDDVYCSFGCLGTYSHTVSYDKC-EVPSNTFNY 178
QY 172 LLIQKG-NATHDVC-----SGNREATQKCGIDVTL---CEAF--FRFAPPTKIIIPNW 219
DB 179 IDVEINLYPVNDISCTRTTGTGSESISTSELTITMNHKDCDPVFRDGYPSVLNKVATSG 238
QY 220 LSVLVDSLPG-TVNAESVE-RIKRRHSSQEQTFOLKLMKHONRDOEW-KKIIDIDL 276
DB 239 FFTGQRYONISKVCTLNFEIKCNKNDSSSKO-----LTKAKNDALIMPSETVTLVGD 292
QY 277 CESSVQRHLGHSNLTE 293
DB 293 CLSSVDIYILYSTNTQ 309

Search completed: December 27, 2000, 10:52:38
Job time: 69 sec

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Result	Score	Query	Match	Length	DB	ID	Description
1	314	14.4	459	2	148854	gene murine tumour	
2	312	14.3	461	1	A35356	tumor necrosis fac	
3	312	14.3	474	2	B38634	tumor necrosis fac	
4	270	12.4	289	2	A46515	B cell-associated	
5	270	12.4	305	2	A46476	B cell-associated	
6	261	12.0	277	2	A60771	B-cell activation	
7	244	11.2	435	2	I54182	tumor necrosis fac	
8	233.5	10.7	325	2	B43662	T2 protein - rabb	
9	220	10.1	326	1	GOVZML	12 protein - myxo	
10	217	10.0	349	2	D36858	gene GAR protein -	
11	216	9.9	348	2	D72175	G2R protein - vari	
12	215.5	9.9	348	2	T28633	hypothetical prote	
13	199	9.1	427	1	GOHUN	nerve growth fact	
14	197.5	9.1	425	1	A26431	nerve growth fact	
15	184	8.4	416	1	JN0006	nerve growth fact	
16	182	8.4	335	2	A40036	apoptosis-mediat	
17	179.5	8.2	314	2	I37383	FAS soluble protei	
18	177	8.1	256	2	B32393	T-cell antigen 4-1	
19	167	7.7	255	2	I38426	4-1B8 - human	
20	166	7.6	255	2	JT0752	lymphocyte activa	
21	165.5	7.6	461	2	JC4302	tumor necrosis fac	
22	163	7.5	271	2	SI2783	OX40 antigen prec	
23	161.5	7.4	454	1	GOMST1	tumor necrosis fac	
24	161.5	7.4	454	2	I57826	tumor necrosis fac	
25	160	7.3	455	1	GOHUT1	tumor necrosis fac	
26	153	7.0	461	1	GORTU1	tumor necrosis fac	
27	152.5	7.0	272	2	I48700	gene OX40 protein	
28	151	6.9	277	2	I37552	OX40 homolog - hu	
29	147.5	6.8	324	2	JC2335	Fas antigen prec	

A;Accession: A35356

A:Accession: A35356

A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-461 <SM>
 A:Cross-references: GB:M32315; NID:g189185; PIDN:AAA59929.1; PID:g189186
 R:Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; Kling, M.W.; Hale, K.K.; Squires, Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990
 A:Title: A second tumor necrosis factor receptor gene product can shed a naturally occur
 A:Reference number: A36475; MUID:91045591
 A:Accession: A36475
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-195, 'R', 197-461 <KOH>
 A:Cross-references: GB:M55994; GB:M38549; NID:g339757; PIDN:AAA36755.1; PID:g339758
 R:Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M. Cytokine 2, 231-237, 1990
 A:Title: Two human TNF receptors have similar extracellular, but distinct intracellular, A:Reference number: A48416; MUID:91370690
 A:Accession: A48416
 A:Status: preliminary
 A:Molecule type: mRNA; protein
 A:Residues: 23-461 <DEM>
 A:Cross-references: GB:S63368; NID:g235648; PIDN:AA19824.1; PID:g235649
 A:Title: Sequence extracted from NCBI Backbone (NCBI:63368, NCBI:63371)
 R:Heiler, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M. Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990
 A:Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demostre
 A:Reference number: A36007; MUID:90349572
 A:Accession: A36007
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 118-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HELE>
 A:Cross-references: GB:M35857; NID:g339751; PIDN:AA6362.1; PID:g339752
 R:Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M. J. Biol. Chem. 265, 20131-20138, 1990
 A:Title: Purification and partial amino acid sequence analysis of two distinct tumor nec
 A:Reference number: A23666; MUID:91056048
 A:Accession: A23666
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 23-40, 65-69, 136-141, 300-306 <OE>
 R:Engelmann, H.; Novick, D.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215
 A:Accession: A35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R:Kunert, P.; Kemper, O.; Wallach, D. J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: I38094; MUID:95121934
 A:Accession: I38094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:g666044; PIDN:CAA56324.1; PID:g825701
 A:Gene: GDB:TNFR2
 A:Map position: 1p36.2-1p36.2
 A:Introns: 26/3
 A:Note: the list of introns is incomplete.
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor type 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>

F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Query Match 14.38; Score 312; DB 1; Length 461;
 Best Local Similarity 34.78; Pred. No. 2.3e-14;
 Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
 QY 8 ALVLDIDIEWTQETLPK--YLHDPETGH-----QLCDKCAPGTYLKH 53
 DB 9 ALAVGLEL--WAAAHALPAQVAFPTPAPEPSTCRLERYQTAKMCCSKCPGQAKVF 66
 QY 54 CTVRKRLTLCVPCPDHSTYDSWHTSDECVYCSPVCKELOSVAQECNRTHNRVCECEGRYL 113
 DB 67 CTKTSDTYCDCEDESTYQKNNWVPECLSCGSRSSDDVETQACTRQGNRICTCRPGWYC 126
 QY 114 EI-----EFLKHSRCPGSGGVQAGTPENNTYCKKPPDPFGSGEYSKAPCIKHNTCS 167
 DB 127 ALSKQEGCRLCAPLKKCPGPGVAPGPTSDVYCKPCAPGTFSTTSSTDICRPHOICN 186
 QY 168 TFGLLLIQGNATHDNVCS 186
 DB 187 VVAL-----PGNMSDAVCT 201
 RESULT 3
 B38634
 tumor necrosis factor receptor type 2 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 30-Jun-1992 #sequence, revision 30-Jun-1992 #text, change 23-Jul-1999
 C:Accession: B38634; A40254; S54816
 R:Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991
 A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis facto
 A:Reference number: A38634; MUID:91187885
 A:Accession: B38634
 A:Molecule type: mRNA
 A:Residues: 1-474 <LEM>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Goodwin, R.S.; Anderson, D.; Jerry, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; J Mol. Cell. Biol. 11, 3020-3026, 1991
 A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors f
 A:Reference number: A40254; MUID:91246168
 A:Accession: A40254
 A:Molecule type: mRNA
 A:Residues: 1-474 <GOO>
 A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828
 R:Krisomergis, M.; Fellows, R.; Feldmann, M.; Chernajovsky, Y. submitted to the EMBL Data Library, May 1995
 A:Description: Characterization of the promoter region of the murine p75-TNF receptor
 A:Reference number: S54816
 A:Accession: S54816
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-22 <KIS>
 A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60618.1; PID:g809044
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: cytokine receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>
 F:40-77/Domain: NGF receptor repeat homology <NG1>
 F:79-120/Domain: NGF receptor repeat homology <NG2>
 F:166-203/Domain: NGF receptor repeat homology <NG4>
 Query Match 14.38; Score 312; DB 2; Length 474;
 Best Local Similarity 34.38; Pred. No. 2.3e-14;
 Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;
 QY 5 LCCALLVLDIDIEWTQETLPKYL--HYDPETGH-----QLCDKCAPGTY 49
 DB 6 LMAVALVEELQ--WATGHTVPAQVAVLPYKPEPGECISOSEYTRDKRQACACCPQOY 63
 QY 50 LKHQTVRKRITLCVPCPDHSTYDSWHTSDECVYCSPVCKELOSVAQECNRTHNRVCECE 109

Db 64 VKHFCKNTSTVACADCAASMTQVWNOFRICLSSSSCTDVOEIRACTKQONVCACEA 123
 QY 110 GRYLEIEF-----CKHRSPPGSGVQAGPERNTVCKKCPDGFSGTSSKAPCIR 162
 Db 124 GRVCAKTKHSGCROCKRLSKCGPGFGVASSRAVNGVNLCKACAPGFSDTSTSDVCRP 183
 QY 163 HTNCTFGLLIIOKGNATHDNCVCS 186
 Db 184 HRICS-----ITAIPIGNASTDAYCA 203

RESULT 4

B cell-associated surface molecule CD40, short splice form - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 26-May-2000
 Accession: A46515
 A:Title: J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, J.; Immunol. 149, 3921-3926, 1992
 A:File: Genomic structure and chromosomal mapping of the murine CD40 gene.
 A:Reference number: A46515; M0ID:93094586
 A:Accession: A46515
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: nucleic acid
 A:Residues: 1289 <GRI>
 A:Cross-references: GB:M83312; NID:g1553058; PIDN:AAB08705.1; PID:g1553059; GB:M94126; N
 A:Experimental source: BALB/c, liver
 A:Note: sequence extracted from NCBI backbone (NCBI:P120357)
 C:Comment: For an alternative splice form, see PIR:A46476
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: alternative splicing
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 270; DB 2; Length 289;
 Best Local Similarity 34.5%; Pred. No. 1,1e-11;

Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

QY 27 KYLHYDEPETHQLLDCKCARGTYLKQCTVRRKTLVCPDPHSTYDSMHTSDEC---VYC 83
 Db 30 QYLH-DSQ-----CCDLCQPSRLTSHCTALEKTCQPCDGSFSAQWNRIRCHQHRHC 83
 QY 84 SPVCKELQSYKQECNRTNHNRYCECEGRYL---EIFECLKHSRCPGSGVQAGPERNT 140
 Db 84 EP--NGLRVRKKEGTASDVCTCKEGBHCTSKCEACAOHTPIPGFVEMATEETDT 141
 QY 141 VCKKCPDGFSGTSSKAPCIRKHTNCTFGLLIIOKGNATHDNCV 185
 Db 142 VCHPCVPGFSSNOSLFEKCYPTWTSCEDKNLEVLQKTSQTNVIC 186

RESULT 5

B cell-associated surface molecule CD40, long splice form - mouse
 A:Accession: A46476
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-305 <TOR>
 A:Cross-references: GB:M83312; NID:g1553058
 A:Note: sequence extracted from NCBI backbone (NCBI:N.75206, NCBI:P.75207)
 C:Comment: For an alternative splice form, see PIR:A46515
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: alternative splicing; transmembrane protein
 F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 12.4%; Score 270; DB 2; Length 305;
 Best Local Similarity 34.5%; Pred. No. 1,2e-11;
 Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

QY 27 KYLHYDEPETHQLLDCKCARGTYLKQCTVRRKTLVCPDPHSTYDSMHTSDEC---VYC 83
 Db 30 QYLH-DSQ-----CCDLCQPSRLTSHCTALEKTCQPCDGSFSAQWNRIRCHQHRHC 83
 QY 84 SPVCKELQSYKQECNRTNHNRYCECEGRYL---EIFECLKHSRCPGSGVQAGPERNT 140
 Db 84 EP--NGLRVRKKEGTASDVCTCKEGBHCTSKCEACAOHTPIPGFVEMATEETDT 141
 QY 141 VCKKCPDGFSGTSSKAPCIRKHTNCTFGLLIIOKGNATHDNCV 185
 Db 142 VCHPCVPGFSSNOSLFEKCYPTWTSCEDKNLEVLQKTSQTNVIC 186

RESULT 6

B-cell activation protein CD40 precursor - human
 N:Alternate names: B-cell surface antigen Bp50
 C:Species: Homo sapiens (man)
 C:Date: 03-Jun-1993 #sequence_revision 03-Feb-1994 #text_change 17-Mar-2000
 C:Accession: S04460; A60771
 R:Stamenkovic, I.; Clark, E.A.; Seed, B.
 EMBL J. 8, 1403-1410, 1989
 A:Title: A B-lymphocyte activation molecule related to the nerve growth factor recept
 A:Reference number: S04460; M0ID:89356608
 A:Accession: S04460
 A:Molecule type: mRNA
 A:Residues: 1-277 <STA>
 A:Cross-references: EMBL:X60592; NID:g29850; PID:g29851
 R:Brasch-Andersen, S.; Pallie, S.; Koho, H.; Nika, H.; Aspenstroem, P.; Perlmann, P.
 J. Immunol. 142, 562-567, 1989
 A:Title: Biochemical characteristics and partial amino acid sequence of the receptor-
 A:Reference number: A60771; M0ID:89093941

A:Accession: A60771
 A:Molecule type: protein
 A:Experimental source: Burkitt lymphoma cell line Raj1
 C:Genetics:
 A:Gene: GDB:CD40
 A:Cross-references: GDB:215268; OMIM:109535
 A:Map position: 20q12-20q13.2
 C:Superfamily: CD27 antigen; NGF receptor repeat homology
 C:Keywords: B-cell; glycoprotein; phosphoprotein; surface antigen; transmembrane prot
 F:1-20/Domain: signal sequence #status predicted <Sig>
 F:21-277/Product: B-cell activation protein CD40 #status experimental <MAT>
 F:21-193/Domain: extracellular #status predicted <EXT>
 F:194-215/Domain: transmembrane #status predicted <TM>
 F:216-277/Domain: intracellular #status predicted <CYT>
 F:153,180/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 12.0%; Score 261; DB 2; Length 277;
 Best Local Similarity 33.9%; Pred. No. 4,4e-11;
 Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

QY 29 LHYDPENG-----HQLLDCKCARGTYLKQCTVRRKTLVCPDPHSTYDSMHTSDEC 80
 Db 18 VHEPPRACREKQYLYNSQCCSLQPOKLVSPCTETFEETECPCGESEFLDTWNRETHC 77
 QY 81 ---VYCSPVCKELQSYKQECNRTNHNRYCECEGRYL---EIFECLKHSRCPGSGVQAG 134
 Db 78 HQKRCYCPNNG--LRVQOKTSETDTICCEBGMHCTSEACSCVLRHSCSPGFGVKQIA 135
 QY 135 TPERNTVCKKCPDGFSGTSSKAPCIRKHTNCTFGLLIIOKGNATHDNCV 185
 Db 136 TGVSDTICEPCVPGFSSNVSAAFEKCHPWTSCETKDLVVOOAGTNKRTDVC 186

```
RESULT 7
154182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: 154182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: 154182; MUID:93252381
A:Accession: 154182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; MID:q339761; PIDN:AAA36757.1; PID:q339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 11.2%; Score 244; DB 2; Length 435;
Best Local Similarity 26.9%; Pred. No. 1.1e-09;
Matches 54; Conservative 32; Mismatches 93; Indels 22; Gaps 6;

QY 9 LLVLDITETMTQETLP-----KYLHDPETGHOLLCKCAPGYLYKQHCTVR 57
D 18 VLGLGLLAASOPQAVPPASENQTCRQDEKRYEPQ--HRCSCRCPPGYTSAKCSRI 75
QY 58 RKLICVPCPDHSYTDSDCYVCSFYCKELQSVKQ--ECNRRHNRCCECEGRY--- 112
D 76 RDTVATCATENYNNHMYLYTICQLCRP--CDPYMGLLELAPTSKRKQCRCRQPMFCA 134
QY 113 --LEIEFLKHSRCPGS--GVVQAGTPERNYCKKCPDGFSEGTSSAKPCKIKHTNCSTF 169
D 135 WALECTHCELSDCPGTEAELEKDEVGKGNHCVCCKAGHFONTSSPSRCPHTRCENQ 194
QY 170 GLLIQKGNATHDNYCSGNRE 190
D 195 GLVEAPGTASDITCKNPLE 215

RESULT 8
B43692
T2 protein - rabbit fibroma virus
C:Species: rabbit fibroma virus; Shope fibroma virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C:Accession: B43692
R:Platon, C.; Delange, A.M.; McFadden, G.
Virology 160, 20-30, 1987
A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
A:Reference number: A43692; MUID:87321103
A:Accession: B43692
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-325 <UPT>
A:Cross-references: GB:M17433
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:64-105/Domain: NGF receptor repeat homology <NG2>
F:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 10.7%; Score 233.5; DB 2; Length 325;
Best Local Similarity 31.7%; Pred. No. 4.2e-09;
Matches 59; Conservative 19; Mismatches 91; Indels 17; Gaps 5;

QY 36 GHO-----LLCKCAPGYLYKQHCTVRRKTLCPDHSYTDSDCYVCSFYCKEL 90
D 30 GHDYKDKDLCSCHPRTYASRLCGPSNTVSPEDGFTSTNHAAPACVSCRGPCIGH 89
QY 91 OSVKQECNTHNRVCECEGRYLET-----FCLKHRSRCPGSGVVQAGTPERNYCKK 144
D 109 LKLVLDITETMTQETLP-----KYLHDPETGHOLLCKCAPGYLYKQHCTVR 157
QY 158 RKLICVPCPDHSYTDSDCYVCSFYCKELQSVKQ--ECNRRHNRCCECEGRY--- 212
D 176 RDTVATCATENYNNHMYLYTICQLCRP--CDPYMGLLELAPTSKRKQCRCRQPMFCA 234
QY 213 --LEIEFLKHSRCPGS--GVVQAGTPERNYCKKCPDGFSEGTSSAKPCKIKHTNCSTF 269
D 235 WALECTHCELSDCPGTEAELEKDEVGKGNHCVCCKAGHFONTSSPSRCPHTRCENQ 294
QY 270 GLLIQKGNATHDNYCSGNRE 290
D 295 GLVEAPGTASDITCKNPLE 315

RESULT 9
154182
tumor necrosis factor receptor 2-related protein - human
C:Species: Homo sapiens (man)
C:Date: 24-May-1996 #sequence_revision 24-May-1996 #text_change 17-Mar-2000
C:Accession: 154182
R:Baens, M.; Chaffanet, M.; Cassiman, J.J.; Van den Berghe, H.; Marynen, P.
Genomics 16, 214-218, 1993
A:Title: Construction and evaluation of a hncDNA library of human 12p transcribed sequen
A:Reference number: 154182; MUID:93252381
A:Accession: 154182
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-435 <RES>
A:Cross-references: GB:L04270; MID:q339761; PIDN:AAA36757.1; PID:q339762
C:Genetics:
A:Gene: GDB:LTBR
A:Cross-references: GDB:1230195; OMIM:600979
A:Map position: 12p13.3-12p13.1
A:Superfamily: tumor necrosis factor receptor type 1; NGF receptor repeat homology

Query Match 10.1%; Score 220; DB 1; Length 326;
Best Local Similarity 29.1%; Pred. No. 3.6e-08;
Matches 53; Conservative 24; Mismatches 85; Indels 20; Gaps 5;

QY 39 LLCKCAPGYLYKQHCTVRRKTLCPDHSYTDSDCYVCSFYCKELQSVKQECN 98
D 38 LCGTSCPPGYSASRLCGPSDTCVSCPKNETFTASTNHAAPACVSCRGCTGHLSESQSD 97
QY 99 RTHNRVCECEGRYLET-----FCLKHRSRCPGSGVVQAGTPERNYCKKCPDGFSSG 152
D 98 KTRDVRVCDGSAGNYCLKQGEGRICAPKTCRCPAGYG--VSGHTPTGVCLCKCRITYSD 156
QY 153 ETSSKAPCIKHTNCSTFELLIOKQ-----NATHDNYCSGNREATOKGIDVTL-----CEE 204
D 157 AVSSTETC-----TSSFNYSIVERNLTPVNDTSCCTTAGPNEVYKTSFSTYTLNHTDCC 211
QY 205 AF 206
D 212 VF 213

RESULT 10
D36858
gene G4R protein - variola virus
N:Alternate names: B28R protein (COP)
C:Species: variola virus
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
C:Accession: D36858; S46888; S32385; S35987
R:Blinov, V.M.
submitted to GenBank, November 1992
A:Description: not shown.
A:Reference number: A36859
A:Accession: D36858
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <BLI>
A:Cross-references: GB:M69198; MID:q456758; PIDN:CAA49137.1; PID:q457087
A:Experimental source: strain 1967, ssp. major, isolate ind3
R:Koljkalov, A.A.; Blinov, V.M.; Gytarov, V.V.; Pozdnyakov, S.G.; Chikhlov, V.E.; F
submitted to the EMBL data library, April 1992
A:Description: Nucleotide sequence analysis of the region of variola virus XhoI F O H
```

A:Reference number: 546868
A:Accession: 546868
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-349 <KOI>
A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449
A:Experimental source: strain India-1967, isolate Inds
R.Shchelkunov, S.N.; Blinov, V.M.; Sandakhchev, L.S.
FEBS Lett. 319, 80-83, 1993
A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
A:Reference number: S32385; MUID:93202281
A:Accession: S32385
A:Molecule type: DNA
A:Residues: 31-168 <SHC>
A:Cross-references: EMBL:X69198
A:Experimental source: strain India-1967, ssp. major
C:Genetics:
Gene: G4R
Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
F:62-66/Domain: NGF receptor repeat homology <NG>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 10.0%; Score 217; DB 2; Length 349;
Best Local Similarity 23.2%; Pred. No. 6.2e-08;
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

OY 4 WLCAALLVLDIDIEWTQETLPPKYLHYDPE-TGHQLLCDKCAPGTYLKQHTVRRKTLIC 62
DB 11 FLSCIIINGRODAPYT-----PPNGCKKDTEYKRNNLCCLSCPGETYASRLCDSTNTQC 65
OY 63 VPCPDHSTDSMHSDECVYCSPVCKELQSAVQKQECNFRTHNRYCECEBGRYLEI-----E 116
DB 66 TPCGSGFTSRNNHLPACISCNGRCNSNOVETRSCNTHNHRICECSPGYCLLKGSSGCK 125
OY 117 FCLKRSCPSPGSGVQAGPPEHNTVCKKCPGDFEGEETSSAPKCIKHNCSPFGLLLQ- 175
DB 126 ACVSQTKCGIGG-VSGHTSVGDVICSPCGFGTYSHTVSSADKCEPVDP-NTEFNIDVEI 183
OY 176 KGNATHDVCSGNREATORCQIDVTLCEAEFRFAVPKILIPNMLSVLDSLPGRVNAE 235
DB 184 TLVPYNDISCT-----RTTTTGLSE-----SILSEL----- 210
OY 236 SVERIKRRHS-----QEQFQLK-----LMKHQNDQEMVKIIDDIDCESSVGRH 284
DB 211 ---TITMHTDPCNPVREYFVSLNKVATSGFTEGNRYONISK-----VCLNFEIK 260
OY 285 LGHSULTTEQLLALMESLPCKKISPEELERTKTKSSPOLKILSLMKIRKGDODTLKG 344
DB 261 CNNKGSSEKOLTKAKND--DGMMSSEFVTLAGDCLSVDIILYSNTNAODYETDLS- 317
OY 345 LMYALKHL--KTSHP-----KVTYHSLRKTMREL 372
DB 318 --YRYGNVLDDDSHMPGSCNTHKPIITNS--KPTREL 349

RESULT 11
D72175
G2R protein - variola minor virus (strain Garcia-1966)
C:Species: variola minor virus
C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
C:Accession: D72175
R.Shchelkunov, S.N.; Totemuh, A.V.; Gutorov, V.V.; Safonov, P.F.; Massung, R.F.; Lopatin
submitted to GenBank, March 1998
A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
A:Reference number: A72150
A:Accession: D72175
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-349 <SHC>
A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
A:Experimental source: strain Garcia-1966

C:Genetics:
A:Gene: G2R
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 9.9%; Score 216; DB ?; Length 349;
Best Local Similarity 23.1%; Pred. No. 7,9e-08;
Matches 92; Conservative 51; Mismatches 169; Indels 84; Gaps 17;

QY 4 WLCCALLVLDLIIEMTQETLPPRYLHYDEP-TGHOLLCDKCAPGTYLKQHCIVRRKTL 62
Db 11 FLSCIIINGRAAYT-----PRNGKCKDEYKRRHNLCCLSCSPRGTYASRLCDSKTNQC 65
QY 63 VPCPDHSTDSWHTSDECVYCSPYCKELQSYKQDCNRTNHNVCCEEGRYLET-----E 116
Db 66 TPCCSGITTSNNHLPACLSGRCNCSNOVETRECNTHNHCICSPGYLLGLGSSGCK 125
QY 117 FCLNHRSCPSPSGVQAGTPRNATVCKKCPDGFSGETSSAPCIKHTNCSFGLLIQ- 175
Db 126 ACVSOTKCGIGY-VSGHTSVGDYICSPCGGTYSTVSSIDCKEPPRN-NTFNVIDEI 183
QY 176 KGNATHDVCSGNREATQCKGIDVTYLCGEAFREAVPTKIIIPMLSVLYDSLPGTKVNAE 235
Db 184 TLTYVNDTSCR-----RTTTGLSE-----SILTSEL----- 210
QY 236 SVERIKRRHS-----QEQTFQLK-----LKHONRDEMKVKTIIQDIDLCSSVORH 284
Db 211 ---TITMHTDCNPFREYFESVLNKVATSGFFGNGRYONISK-----VCTLNFEEK 260
QY 285 LGSNLTLEOLLAMESLPKGIISPEIERIKRCKSSEDLKTLISLRKINGQDPTLKG 344
Db 261 CNNGGSSFKQLTKAKND--DGMMSHSEVTLAGCCLSSVDIYLIXSNTMADYETDTIIS- 317
QY 345 LMYALKHL--KTSHP-----KTVTHSLRKTMFEL 372
Db 318 --YRVGNVLDSDSHMPGSCDIHKLITNS--KPTFEL 349

RESULT 12
228623
hypotheical protein g2r - variola major virus
C:Species: variola major virus
C:Date: 22-Oct-1999 #sequence_rev: 22-Oct-1999 #text_change 31-Jan-2000
C:Accession: J28623
R:Massung, R.R.; Esposito, J.J.; Liu, L.I.; Qi, J.; Uterback, T.R.; Knight, J.C.; Au
Nature 366, 748-751, 1993
A>Title: Potential virulence determinants in terminal regions of variola smallpox virus
A:Reference number: 220488; MUID:94088747
A:Accession: J28623
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-348 <MAS>
A:Cross-reference: EMBL:L22579; PIDN:AA60933.1
A:Experimental source: strain Bangladesh 1975
C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 9.9%; Score 215.5; DB 2; Length 348;
Best Local Similarity 23.1%; Pred. No. 7.9e-08;
Matches 87; Conservative 47; Mismatches 156; Indels 87; Gaps 16;

QY 31 YDPETG-----HOLLCDKCAPGTYLKQHCIVRRKTLCPDHSYTDSSWHTSDECV 81
Db 24 YTPNGKCKDEYKRRHNLCCLSCPRGYASRLCDSKTNQCTPCGSGTFISRNHLPACL 83
QY 82 YCSFVCKELQSYKQDCNRTNHNVCCEEGRYLET-----EFLCKHNSCPSPSGVQAGT 135
Db 84 SCNCRCSNOVETSCNTHNHCICSPGYLLGLGSSGCKACACVSQTKGIGY-VSGHT 142
QY 136 PERMTVCKKCPDGFSGETSSKAPCIKHTNCSFGLLIQ-KGNATHDVCSGNREATOR 194
Db 143 SVGDYICSPCGGTYSTVSSIDCKEPPRN-NTFNVIDEITLYPVNDTSC-----RTTT 197

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OY 195 CGIDVTLCEFAFFFAVPTKIIIPMWLSVLDLPCTKVNASEVERIKRRHS-----OEQ 249
D 198 TGLSE-----SILISEL-----TITMNHDCNPVREE 225
OY 250 TFOLEK-----LWKHONRODEMVKKIIODIDLCSSVORHAGHSNLTTEOLALMESLP 303
D 226 YFSLNKNVANSGETGNGRKNISK-----VCTLINEICNNKSGSFOLTLAKND-- 276
OY 304 GKKSPEIEFTKRTCKSSSEDLKLSLWRIKNGDDTLKALTKLHL--KTSHP-- 358
D 277 DGMMSHEVTLACDCLISVDIYILYSNTNADYETDITIS---YRGNVLDLDDSHMPSGC 333
OY 359 ---KTWTHSLKRTMRFL 372
D 334 NIKPITNS--KPTREFL 348

RESULT 13
GOHUN
Nerve growth factor receptor precursor, low affinity - human
N:Alternate names: NGF receptor
C:Species: Homo sapiens (man)
Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 22-Jun-1999
C:Accession: A25218; A60204; S21689; I57638
R:Johnson, D.; Iannan, A.; Buck, C.R.; Sehgal, A.; Morgan, C.; Mercer, E.; Bothwell, M.
Cell 47, 545-554, 1986
A:Title: Expression and structure of the human NGF receptor.
A:Reference number: A25218; MUID:87051725
A:Accession: A25218
A:Molecule type: mRNA
A:Residues: 1-427 <JOH>
A:Cross-references: GB:M14764; NID:g189204; PIDN:AA59544.1; PID:g189205
R:Mariano, N.; Dietzschold, B.; Earley Jr., J.J.; Schattelman, G.; Thompson, S.; Grob, P.;
J. Neurochem. 48, 225-232, 1987
A:Title: Purification and amino terminal sequencing of human melanoma nerve growth factor
A:Reference number: A60204; MUID:87085574
A:Accession: A60204
A:Molecule type: protein
A:Residues: 29-31,'R',33-42,'RR',45-46,'RX',50-51,'XX',54-56 <MAR>
A:Experimental source: melanoma cell line A875
A:Note: This sequence has been corrected by a note added in proof to follow the nucleotide
R:Yissavajhala, P.; Leszyk, J.D.; Lin-Goetze, J.; Ross, A.H.
Arch. Biochem. Biophys. 294, 244-252, 1992
A:Title: Structural domains of the extracellular domain of human nerve growth factor
A:Reference number: S21689; MUID:92198017
A:Accession: S21689
A:Status: preliminary
A:Molecule type: protein
A:Residues: 183-208 <VIS>
R:Sehgal, A.; Patel, N.; Chao, M.
Cell. Biol. 8, 3160-3167, 1988
A:Title: A constitutive promoter directs expression of the nerve growth factor receptor
A:Reference number: I57638; MUID:89096903
A:Accession: I57638
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-22 <RES>
A:Cross-references: GB:M21621; NID:g189206; PIDN:AA3363.1; PID:g189207
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Comment: This protein is thought to form a high-affinity receptor when it associates
C:Comment: This receptor undergoes both N- and O-linked glycosylation.
C:Genetics:
A:Gene: GDB:NGFR
A:Cross-references: GDB:120234; OMIM:162010
A:Map position: 17q21-17q22
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor;
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-47/Domain: nerve growth factor receptor #status experimental <MAT>
F:29-250/Domain: extracellular #status predicted <EXT>
F:32-65/Domain: NGF receptor repeat homology <NG1>
F:67-108/Domain: NGF receptor repeat homology <NG2>

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F:109-147/Domain: NGF receptor repeat homology <NG3>
F:149-189/Domain: NGF receptor repeat homology <NG4>
F:197-248/Domain: serine/threonine-rich
F:251-272/Domain: transmembrane #status predicted <TM>
F:273-427/Domain: intracellular #status predicted <INT>
F:60/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 199; DB 1; Length 427;
Best Local Similarity 31.7%; Pred. No. 1,4e-06;
Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;

OY 9 LTVLIDIIEMTQETLPKYLHYDPETGHQLCDKCAPGYTLKQHCVRKRTLCVCPFDH 68
D 17 LLLGLVSLGAKKACPTGLTHSGE-----CKACMLGEGVAKQPCGA-NQYCEPCLDS 70
OY 69 -SYDSWHTSDECVYCSPVCKELQSVKQECNRTNRYCEDEEGRYLE-----IEFCIKHR 122
D 71 VTFSDVVSATEPKPCPE-CVGLQSMGAPCEVADDAVCRCAYGYODETTRCEAC---R 126
OY 123 SCPPGSGVQAQGPRTNVCCKCPDFGSEFTSSKAPCIRHTNC 166
D 127 VCEAGSGLVFSCDQKNTVCECPDGYSDANHVDPCLPCTVC 170

RESULT 14
A26431
Nerve growth factor receptor precursor, low affinity - rat
N:Alternate names: NGF receptor
C:Species: Rattus norvegicus (Norway rat)
Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: A26431; PH1229
R:Raddeke, M.T.; Misko, T.P.; Hsu, C.; Herzenberg, L.A.; Shooter, E.M.
Nature 325, 593-597, 1987
A:Title: Gene transfer and molecular cloning of the rat nerve growth factor receptor.
A:Reference number: A26431; MUID:87115859
A:Accession: A26431
A:Molecule type: mRNA
A:Residues: 1-425 <RAD>
A:Cross-references: GB:X05137; NID:g56755; PIDN:CA28783.1; PID:g56756
R:Meisls, M.; Timmusk, T.; Allikmets, R.; Saarma, M.; Persson, H.
Gene 121, 247-254, 1992
A:Title: Regulatory elements and transcriptional regulation by testosterone and retin
A:Reference number: PH1229; MUID:93077038
A:Accession: PH1229
A:Molecule type: DNA
A:Residues: 1-20 <MET>
A:Cross-references: GB:X61269
C:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastom
C:Comment: The cysteine-rich region of the extracellular domain may form part or all
C:Comment: This protein is thought to form a high-affinity receptor when it associate
C:Genetics:
A:Insertions: 20/3
C:Superfamily: nerve growth factor receptor; NGF receptor repeat homology
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor
F:1-29/Domain: signal sequence #status predicted <SIG>
F:30-425/Product: nerve growth factor receptor #status predicted <EXT>
F:30-221/Domain: extracellular #status predicted <EXT>
F:33-66/Domain: NGF receptor repeat homology <NG1>
F:68-109/Domain: NGF receptor repeat homology <NG2>
F:110-148/Domain: NGF receptor repeat homology <NG3>
F:150-190/Domain: NGF receptor repeat homology <NG4>
F:198-249/Domain: serine/threonine-rich
F:252-273/Domain: transmembrane #status predicted <MEM>
F:274-425/Domain: intracellular #status predicted <INT>
F:61/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.1%; Score 197.5; DB 1; Length 425;
Best Local Similarity 22.1%; Pred. No. 1.7e-06;
Matches 95; Conservative 59; Mismatches 152; Indels 123; Gaps 19;

OY 9 LTVLIDIIEMTQETLPKYLHYDPETGHQLCDKCAPGYTLKQHCVRKRTLCVCPFDH 68

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Db 18 LLLILGSSGAKRKTCTGLYTHSGE-----CCACACNGBEAVAPCGA-NQTVCEPCLDN 71
QY 69 -SYDSMHTSDEVCYSPVCKELOSVKQECNRTHNRYCECEBGRYLEIE--FCLKHNSCP 125
Db 72 VTFSDVVSATPECPKPTCE-CIGLOSMASAPCAVEADAVRCARAGYQDEDETHCEACSVCE 130
QY 126 PGSGVYAGTPERTNVCKKCGDFFSGTSSKAPCIRKNTSGFLLIIOGKNAHDNVC 185
Db 131 VGSGLVSCODKONTVCECEGEGTYSDEANHVDPCLPCTVEDTEROL----- 178
QY 186 SGNREATOKGIDVTLCSEAFRR-----AVPRK--IIPNMLSVL 223
Db 179 ---RECTPMADAE---CEIIGRWIPRSTPREGSDTAPSTQEBEVPEPQDLVSTVADM 232
QY 224 VDSLPGTRVNAESVERIKRRHSQD-----QTFOLKLWK--HONRDOE 265
Db 233 VTTVMG-----SSQPVYTRGTDLNLIPIVYCSILAAVYVGLVAYIAFRMNSCKONKQGA 286
QY 266 MVKKIIQ-----DIDCESSVQRHLGHSNLTTFQLLA---LMESLPGRK-- 306
Db 287 NSRPVNOTPPEGEKLSHSDSGISVDSQSLHDQHTOTQASGALKGDGNTLXSLPTKRE 346
QY 307 -----ISPEIER-TRKCKSSQQLKLSLRIRKNGDQD--TLKG 344
Db 347 EVELKNGDTRHRLAGELGYQPEHIDSTHEAC-----PYRALLSW-----GADSATLDA 398
QY 345 LMYALKHLK 353
Db 399 LLAALRRIQ 407

```

RESULT 15

```

JN0006
nerv growth factor receptor, low affinity precursor - chicken
N:Alternate names: NGF receptor
C:Species: Gallus gallus (chicken)
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: JN0006; A60504
R:Large, T.H.; Meskamp, G.; Helder, J.C.; Radeke, M.J.; Misko, T.P.; Shooter, E.M.; Reid
Neuron 2, 1123-1134, 1989
A:Title: Structure and developmental expression of the nerve growth factor receptor in t
A:Reference number: JN0006; MUID:90165579
A:Accession: JN0006
A:Molecule type: mRNA
R:Residues: 1-416 <LAR>
Experimental source: embryonic chick brain
Heuer, J.G.; Fatemie-Nainie, S.; Wheeler, E.F.; Bothwell, M.
Dev. Biol. 137, 287-304, 1990
A:Title: Structure and developmental expression of the chicken NGF receptor.
A:Reference number: A60504; MUID:90152140
A:Accession: A60504
A:Molecule type: mRNA
A>Status: preliminary; not compared with conceptual translation
A:Comment: This receptor is found on sensory and sympathetic neurons, on neuroblastoma c
C:Comment: The cysteine-rich region of the extracellular domain may form part or all of
C:Superfamily: This protein is thought to form a high-affinity receptor when it associates w
C:Keywords: duplication; glycoprotein; heterodimer; monomer; phosphoprotein; receptor; t
F:1-20/Domain: signal sequence #status predicted <SIG>
F:21-416/Product: nerve growth factor receptor #status predicted <MAT>
F:21-239/Domain: extracellular #status predicted <EXT>
F:24-57/Domain: NGF receptor repeat homology <NG1>
F:59-100/Domain: NGF receptor repeat homology <NG2>
F:101-139/Domain: NGF receptor repeat homology <NG3>
F:141-181/Domain: NGF receptor repeat homology <NG4>
F:189-237/Region: serine/threonine-rich
F:240-261/Domain: transmembrane #status predicted <MEM>
F:262-416/Domain: intracellular #status predicted <INT>
F:52/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match      8.4%; Score 184; DB 1; Length 416;
Best local similarity 30.9%; Pred. No. 1.4e-05;
Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

QY 41 CDKCAPGTLYKQHCTVRRKTLVCPDH-SYDSMHTSDEVCYSPVCKELOSVKQECNR 99
Db 36 CKACNLBEGVYQPCGV-NQTVCEPCLDVSYSDVVSATPECPKPTQ-CVGLHSMAPC 93
QY 100 THNRYCECEBGRYLEIE---CLKHNSCPGSGVYQAGTPERTNVCKKCPDGFSGETS 156
Db 94 SDAVYCRQAYG-YFQDELSGSCKECSICEVGFGLMFPQRSDTVCEBCEGTFESDANF 152
QY 157 KAPCIRKHTNCSFGLLIIOGKNAHDNVC 185
Db 153 VDPCLPCTICEE-NEVMKECTATSDAEC 180

```

Search completed: December 27, 2000, 10:54:37
 Job time: 188 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:38 ; Search time 24.16 Seconds
(without alignments)
530.262 Million cell updates/sec

Title: US-09-389-545-2

Sequence: 1 MNKWLCCALLVLDIIEWT.....OKFLFMIGNOVSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Archived: 87993 segs, 31947931 residues

Total number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database: SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	314	14.4	461	1	TNR2_HUMAN
2	312	14.4	474	1	TNR2_MOUSE
3	270	12.4	289	1	CD40_MOUSE
4	261	12.0	277	1	CD40_HUMAN
5	244	11.2	435	1	TNRC_HUMAN
6	233.5	10.7	335	1	VT2_SFVRA
7	228	10.5	259	1	CD40_BOVIN
8	220	10.1	349	1	VT2_MXYVL
9	217	10.0	349	1	VC22_VAVR
10	206	9.5	415	1	TNRC_MOUSE
11	199	9.1	427	1	NGFR_HUMAN
12	197.5	9.1	425	1	NGFR_RAT
13	190.5	8.7	323	1	FASA_BOVIN
14	184	8.4	416	1	NGFR_CHICK
15	182	8.4	335	1	FASA_HUMAN
16	177	8.1	256	1	41BB_MOUSE
17	176	8.1	332	1	FASA_PIG
18	167	7.7	255	1	41BB_HUMAN
19	165.5	7.6	461	1	TNR1_PIG
20	163	7.5	271	1	OX40_RAT
21	161.5	7.4	454	1	TNR1_MOUSE
22	160	7.3	455	1	TNR1_HUMAN
23	160	7.3	471	1	TNR1_BOVIN
24	153	7.0	461	1	TNR1_RAT
25	152.5	7.0	272	1	OX40_MOUSE
26	151	6.9	277	1	OX40_HUMAN
27	147.5	6.8	324	1	FASA_RAT
28	143	6.6	327	1	FASA_MOUSE
29	139	6.4	395	1	CD30_HUMAN
30	133	6.1	1786	1	LMB1_HUMAN
31	130.5	6.0	1789	1	LMB1_DROME
32	126.5	5.8	260	1	CD27_HUMAN
33	125	5.7	1680	1	FUR2_DROME

34	120.5	5.5	250	1	CD27_MOUSE	P41272 mus musculu
35	120.5	5.5	291	1	FBN2_HUMAN	P35556 homo sapien
36	119.5	5.5	1639	1	LMG1_DROME	P15215 drosophila
37	119	5.5	1609	1	LMG1_HUMAN	P11047 homo sapien
38	118	5.4	3712	1	LMA_DROME	000174 drosophila
39	116.5	5.3	915	1	PAC6_MOUSE	004592 mus musculu
40	116	5.3	1955	1	AGRI_CHICK	P31696 gallus gall
41	116	5.3	3084	1	LMAI_MOUSE	P19137 mus musculu
42	116	5.3	3106	1	LMAI_MOUSE	Q60675 mus musculu
43	115.5	5.3	713	1	TS4A_GIALA	P21849 giardia lam
44	115.5	5.3	1607	1	LMG1_MOUSE	P02468 mus musculu
45	115	5.3	417	1	MSL1_HUMAN	Q93038 h wal-1 pro

ALIGNMENTS

RESULT	ID	SEQUENCE	STANDARD	PRT	AA
1	TNR2_HUMAN				
1	TNR2_HUMAN				
AC	P20333				
DT	01-FEB-1991 (Rel. 17, Created)				
DT	01-AUG-1991 (Rel. 19, Last sequence update)				
DT	01-OCT-2000 (Rel. 40, Last annotation update)				
DE	TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TUMOR NECROSIS FACTOR BINDING PROTEIN 2) (TNFRI) (P80) (TNF-R2) (CD120B) (ETANERCEPT)				
GN	TNFRSF1B OR TNFR2 OR TNFR				
OS	Homo sapiens (Human)				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 90260639.				
RA	Smith C.A., Javits T., Anderson D., Solam L., Beckmann M.P., Jerzy R., Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;				
RT	"A second tumor necrosis factor receptor gene product can shed a naturally occurring tumor necrosis factor inhibitor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE: 96299745.				
RA	Beitinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J., Lepailler D., Stallard B.J., Goeddel D.V., Desauvage F.J.;				
RT	"Physical mapping and genomic structure of the human TNFR2 gene.";				
RL	Genomics 35:94-100(1996).				
RN	[4]				
RP	SEQUENCE OF 116-461 FROM N.A., AND PARTIAL SEQUENCE.				
RX	MEDLINE: 90349572.				
RA	Heiler R.A., Song K., Onasch M.A., Fischer W.H., Chang D., Ringold G.M.;				
RT	"Complementary DNA cloning of a receptor for tumor necrosis factor and demonstration of a shed form of the receptor.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).				
RN	[5]				
RP	SEQUENCE OF 27-31.				
RX	MEDLINE: 90110215.				
RA	Engelman H., Novick D., Wallach D.;				
RT	"Two tumor necrosis factor-binding proteins purified from human urine. Evidence for immunological cross-reactivity with cell surface tumor necrosis factor receptors.";				
RL	J. Biol. Chem. 265:1531-1536(1990).				
RN	[6]				
RP	SEQUENCE OF 22-40: 65-69; 136-141; 300-306 AND 346-362.				
RX	MEDLINE: 91056048.				

RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,
 RA Brockhaus M.,
 RT "Purification and partial amino acid sequence analysis of two
 RT distinct tumor necrosis factor receptors from HL60 cells.",
 RL J. Biol. Chem. 265:20131-20138(1990).
 RP [7]
 RP CHARACTERIZATION.
 RX MEDLINE: 93016040.
 RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,
 RA Lipari M.T., Goeddel D.V.,
 RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.
 RT Characterization of ligand binding, internalization, and receptor
 RT phosphorylation.",
 RL J. Biol. Chem. 267:21172-21178(1992).
 RN [8]
 RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN TNF2 COMPLEX.
 RX MEDLINE: 99221490.
 RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.,
 RT "Structural basis for self-association and receptor recognition of
 RT human TNF2.",
 RL Nature 398:533-538(1999).
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA. HIGH AFFINITY FOR TNA-ALPHA AND
 CC APPROXIMATELY 5-FOLD LOWER AFFINITY FOR TNF-BETA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: PHOSPHORYLATED; MAINLY ON SERINE RESIDUES WITH A VERY LOW
 CC LEVEL ON THREONINE RESIDUES.
 CC -1- PHARMACEUTICAL: AVAILABLE UNDER THE NAME ENBREL (IMMUNEX AND
 CC WEITH-AYENST). USED TO TREAT MODERATE TO SEVERE RHEUMATOID
 CC ARTHRITIS (RA). ENBREL CONSIST OF THE EXTRACELLULAR LIGAND-BINDING
 CC PORTION OF TNF2 LINKED TO AN IMMUGLOBULIN FC CHAIN. IT BINDS TO
 CC TNF-ALPHA AND BLOCKS ITS INTERACTIONS WITH RECEPTORS.
 CC -1- SIMILARITY: CONTAINS A LA-NGRP/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- DATABASE: NAME-PROV, NOTE-CD guide CD120b entry;
 CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD120B.HTM"
 CC -1- DATABASE: NAME-Enbrel; NOTE-Clinical information on Enbrel;
 CC WWW="HTTP://WWW.ENBRELINFO.COM/".
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M32315; AAA59929.1; -;
 DR EMBL: M38857; AAA63262.1; -;
 DR EMBL: U52165; AAC50622.1; JOINED.
 DR EMBL: U52156; AAC50622.1; JOINED.
 DR EMBL: U52157; AAC50622.1; JOINED.
 DR EMBL: U52158; AAC50622.1; JOINED.
 DR EMBL: U52159; AAC50622.1; JOINED.
 DR EMBL: U52160; AAC50622.1; JOINED.
 DR EMBL: U52161; AAC50622.1; JOINED.
 DR EMBL: U52162; AAC50622.1; JOINED.
 DR EMBL: U52163; AAC50622.1; JOINED.
 DR EMBL: U52164; AAC50622.1; JOINED.
 DR EMBL: M55994; AAA36755.1; -;
 DR PIR: A35356; A35356.
 DR PIR: A36007; A36007.
 DR PIR: A36475; A36475.
 DR PIR: B35010; B35010.
 DR PIR: A23666; A23666.
 DR PDB: 1CA9; 12-APR-99.
 DR MIM: 191191; -;
 DR INTERPRO: IPR001368; -;
 DR PFM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS00500; TNFR_NGFR_2; 4.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal;
 KW Phosphorylation; Pharmaceutical; 3D-structure.
 FT SIGNAL 1 22
 FT CHAIN 23 461 TUMOR NECROSIS FACTOR RECEPTOR 2.

FT DOMAIN 23 257
 FT TRANSMEM 258 287
 FT DOMAIN 288 461
 FT DOMAIN 39 201
 FT REPEAT 39 76
 FT REPEAT 77 118
 FT REPEAT 119 162
 FT REPEAT 163 201
 FT DISULFID 40 53
 FT DISULFID 54 67
 FT DISULFID 57 75
 FT DISULFID 78 93
 FT DISULFID 96 110
 FT DISULFID 100 118
 FT DISULFID 120 126
 FT DISULFID 134 143
 FT DISULFID 137 161
 FT DISULFID 164 179
 FT CARBOHYD 171 171
 FT CARBOHYD 193 193
 FT CONFLICT 141 141
 FT CONFLICT 196 196
 FT CONFLICT 363 363
 FT SEQUENCE 461 AA; 48316 MM; 603B580BCD67636F CRC64;
 Query Match 14.4%; Score 314; DB 1; Length 461;
 Best Local Similarity 34.7%; Pred. No. 1,9e-15;
 Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;
 OY 8 ALVYLDIDIEWTQETLPPK--YLHDPETGH-----QLLDKCAPGTYLKOH 53
 DB 9 ALAVGLEL--AAAHALPAQVAFTPYADPEPSTCRLEAYDQTQNMCKSCSPGQHKVF 66
 OY 54 CTVRRTLCVPCPHSYSDTSWHTSDECVYCSPVCKELQSVKQECNFRTHRVCEBEGRYL 113
 DB 67 CKTSDFVDCSDCEDSTYQLQNMWPECLSCGSCSSQVETQACTREQNRICTCRPGWYC 126
 OY 114 EI-----EPLKTRSCPPSGGVQAGPRPNYCKKCPDGFSEGSRAKPCIKHTNCS 167
 DB 127 ALSQEGCRLLAPLKKCPGFGVAPGTETSDVYCKPCAPGTFSNTTSSIDICRPHQICN 186
 OY 168 TFGLLDIGNGNATHDNYCS 186
 DB 187 VVAI-----PGNASRDVCT 201
 RESULT 2
 ID TNFR_MOUSE STANDARD; PRT; 474 AA.
 AC P25119; P97893;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE TUMOR NECROSIS FACTOR RECEPTOR 2 PRECURSOR (TNF-R2) (P75).
 GN TNFRSF1B OR TNFR2 OR TNFR-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 91187885.
 RA Lewis M., Tartaglia L.A., Lee A., Bennett G.L., Rice G.C.,
 RA Wong G.H., Chen E.Y., Goeddel D.V.,
 RT "Cloning and expression of cDNAs for two distinct murine tumor
 RT necrosis factor receptors demonstrate one receptor is species
 RT specific.",
 RL Proc. Natl. Acad. Sci. U.S.A. 88:2830-2834(1991).
 RN [2]
 RN SEQUENCE FROM N.A.
 RP MEDLINE: 91246168.
 RX Goodwin R.G., Anderson D., Jerzy R., Davis T., Brannan C.I.,
 RA Copeland N.G., Jenkins N.A., Smith C.A.,

"Molecular cloning and expression of the type 1 and type 2 murine RT receptors for tumor necrosis factor.";
 RL Mol. Cell. Biol. 11:3020-3026(1991).
 RN [3]
 RP SEQUENCE OF 1-26 FROM N.A.
 RC STRAIN-NOD;
 RA Jacob C.O., Liu J.;
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE-LIVER;
 RA Kissenberghs M., Fellnowes R., Feldmann M., Chernaiovsky Y.;
 RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: RECEPTOR FOR TNF-ALPHA.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC -----
 CC EMBL: M60459; AAA39752.1; -
 DR EMBL: M59378; AAA40463.1; -
 DR EMBL: U39488; AAA85021.1; -
 DR EMBL: X87128; CAA60618.1; -
 DR PIR: B38634; B38634.
 DR HSSP: P19438; 1NCF.
 DR MGD: MGI:1314883; TNFRSF1B.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 22
 FT CHAIN 23 474
 FT DOMAIN 23 258
 FT TRANSMEM 259 288
 FT DOMAIN 289 474
 FT DOMAIN 39 203
 FT REPEAT 39 77
 FT REPEAT 78 119
 FT REPEAT 120 164
 FT REPEAT 165 203
 FT DISULFID 40 54
 FT DISULFID 55 68
 FT DISULFID 58 76
 FT DISULFID 79 94
 FT DISULFID 97 111
 FT DISULFID 101 119
 FT DISULFID 121 127
 FT DISULFID 136 145
 FT DISULFID 139 163
 FT DISULFID 166 181
 FT CARBOHYD 69 69
 FT CARBOHYD 195 195
 FT SEQUENCE 474 AA; 50319 MW; 462EAE398CAD563 CRC64;
 Query Match 14.3%; Score 312; DB 1; Length 474;
 Best Local Similarity 34.3%; Pred. No. 2.8e-15;
 Matches 70; Conservative 22; Mismatches 84; Indels 28; Gaps 5;

OY 110 GRLEIEF-----CLKHSQPGSGYVQAGTPENTYCKKPCDFSGSSKAPCIK 162
 Db 124 GRYCAKTHSGSCROCMRLSKGPGFGVASSRAPNGNVILCKACAPCTFSDTTSSTVCRP 183
 OY 163 HTNGSTFGLLIQGNATHDNVCS 186
 Db 184 HRICS-----ILAIPTGNASTDAVCA 203
 RESULT 3
 CD40_MOUSE STANDARD; PRT; 289 AA.
 ID CD40_MOUSE
 AC P27512;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE CD40: RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDW40).
 GN TNFRSF5 OR CD40.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 92105763.
 RA Torres R.M., Clark E.A.;
 RT "Differential increase of an alternatively polyadenylated mRNA
 RT species of murine CD40 upon B lymphocyte activation."
 RL J. Immunol. 148:620-626(1992).
 RN [2]
 RP REVISIONS.
 RC STRAIN-BALB/C;
 RA Torres R.M.;
 RL Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/C; TISSUE-LIVER;
 RX MEDLINE: 93094586.
 RA Grimaldi J.C., Torres R., Kozak C.A., Chang R., Clark E.A.,
 RA Howard M., Cockayne D.A.;
 RT "Genomic structure and chromosomal mapping of the murine CD40 gene."
 RL J. Immunol. 149:3921-3926(1992).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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 CC -----
 CC EMBL: M83312; AAB08705.1; -
 DR EMBL: M94126; AAA37404.1; -
 DR EMBL: M94129; AAA37404.1; JOINED.
 DR EMBL: M94128; AAA37404.1; JOINED.
 DR EMBL: M94127; AAA37404.1; JOINED.
 DR PIR: A46476; A46476.
 DR HSSP: P25942; 1CDF.
 DR MGD: MGI:88336; TNFRSF5.
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 DR KW Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1 19
 FT CHAIN 20 289
 FT DOMAIN 20 193
 FT TRANSMEM 194 215
 FT DOMAIN 216 289
 FT DOMAIN 225 187
 FT SEQUENCE 225 AA; 4 X TNFR-CYS.

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FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 289 AA; 32111 MM; C791CB6D2FEA574E CRC64;

Query Match 12.4%; Score 270; DB 1; Length 289;
Best Local Similarity 34.5%; Fred. No. 1.5e-12;
Matches 57; Conservative 26; Mismatches 68; Indels 14; Gaps 5;

OY 27 KYLHDPETGHQLDDCKAPGTYLKHOCVRRKTLCPDPDSHYDSMTSEDC--VYC 83
Db 30 OYLH-DGQ-----CCDLCPGSRSLSHCTALKEKTOCHPCDSESEFSAQNNRELRCHOHRC 83
OY 84 SPVCKELOSVKOEKNRTHNRNVCCEBGRY--ETIEFCLKHSRCPGSGVVOAGTPERNT 140
Db 84 EP--NQLARKVKEGTAESDVTCTCKEKGCHTSKDEACAGQHPCIPGFGVMATETDT 141
OY 141 VCKKCPDGFSGEITSKAPCIHTNCSITFGLLIIOGNATHNVNC 185
Db 142 VCHPCPVGFFSNOSLSIFKCYPMPTSCEDKNLEVLQKTSQITNVIC 186

RESULT 4
CD40_HUMAN STANDARD; PRT; 277 AA.
ID CD40_HUMAN
AC P25942;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (BP50) (CDM40)
DE (TUMOR NECROSIS FACTOR RECEPTOR 5).
GN TNFRSF5 OR CD40.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN [1]
RX MEDLINE; 89356608.
RA Stamenkovic I., Clark E.A., Seed B.;
RT "A B-lymphocyte activation molecule related to the nerve growth
RL factor receptor and induced by cytokines in carcinomas.";
RL EMBL J. 8:1403-1410(1985).
RN [2]
RX MEDLINE; 97189482.
RA Bajorath J., Aruffo A.;
RX "Construction and analysis of a detailed three-dimensional model of
RL the ligand binding domain of the human B cell receptor CD40.";
RN [3]
RX MEDLINE; 98266353.
RA Singh U., Gardner E., van Vlijmen H., Karpusas M., Hsu Y.-M.,
RA Zhang Z., Nasmith J.H., Thomas D.;
RT "The role of polar interactions in the molecular recognition of CD40L
RL with its receptor CD40.";
RL Protein Sci. 7:1124-1135(1998).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- TISSUE SPECIFICITY: B-CELLS AND IN PRIMARY CARCINOMAS.
CC -1- SIMILARITY: CONTAINS A LA-NGRF/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME=PROT; NOTE=CD guide CD40 entry;
CC WWW="HTTP://WWW.NCBI.NLM.NIH.GOV/PROT/CD/CD40.HTM".
CC -----
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DR      EMBL, X60592; CAA43045.1; -.
DR      PIR, S04460; S04460.
DR      PDB, 1CDF; 01-APR-97.
DR      MIM, 109535; -.
DR      INTERPRO: IPR001368; -.
DR      PFAM: PF00020; TNFR_C6; 4.
DR      PROSITE: PS00652; TNFR_NGFR_1; 1.
DR      PROSITE: PS50050; TNFR_NGFR_2; 4.
KW      Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal;
KW      3D-structure.
FT      SIGNAL          1      19      POTENTIAL.
FT      CHAIN           20      277    CD40L RECEPTOR.
FT      DOMAIN          20      193    EXTRACELLULAR (POTENTIAL).
FT      TRANSMEM        194      215    POTENTIAL.
FT      DOMAIN          216      277    CYTOPLASMIC (POTENTIAL).
FT      DOMAIN          225      187    4 X TNFR-CYS.
FT      REPEAT          25      60      TNFR-CYS 1.
FT      REPEAT          61      103    TNFR-CYS 2.
FT      REPEAT          104      144    TNFR-CYS 3.
FT      REPEAT          145      187    TNFR-CYS 4.
FT      REPEAT          26      37
FT      DISULFID        26      37
FT      DISULFID        38      51
FT      DISULFID        42      59
FT      DISULFID        61      77
FT      DISULFID        83      103
FT      DISULFID        105      119
FT      DISULFID        111      116
FT      DISULFID        125      143
FT      CARBOHYD        153      153
FT      CARBOHYD        180      180
FT      SEQUENCE        277 AA; 30619 MW; BC8776EC2C4A5680 CRC64;
                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
                                         N-LINKED (GLCNAC. . .) (POTENTIAL).
                                         *

Query Match          12.0%; Score 261; DB 1; Length 277;
Best Local Similarity 33.9%; Pred. No. 6,4e-12;
Matches 58; Conservative 23; Mismatches 74; Indels 16; Gaps 4;

OY      29 LHYDETG-----HQLLDKCAPGYLYLKHCTVRRKRLTCLVPCPDHSYDTSWHTSDC 80
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      18 VHPPEPTACREKQYLINSQCCLCPGQKIVSDCTEFETETECFLPGESFEFLDTWNRTHC 77
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      81 ---VYCSVCKELQSVKRDCKNTHRVQCECEGRLL---EIFPCLAKHSCPPGSGVYQAG 134
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      78 HQHKACDNLG--LRVQKGKGTSETPTLTICEGWMHCTSEACSVLHRSCSPGFVKQLA 135
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

OY      135 TPRTVYVCKCPDGFSGSETSKAPICIRKYNCSFGLLIQKNTHPDNYC 185
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
DB      136 TGVSDTICEPCVPGFFSNVSAFECHEWTSCEPTDLYVQAGTKTIDVYC 186
          : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 5
TNRN_HUMAN STANDARD: PRT: 435 AA.
AC      P36941.
DT      01-JUN-1994 (Rel. 29, Created)
DT      01-JUN-1994 (Rel. 29, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      LYMPHOKIN-BETA RECEPTOR PRECURSOR (TUMOR NECROSIS FACTOR RECEPTOR
DE      2 RELATED PROTEIN) (TUMOR NECROSIS FACTOR C RECEPTOR).
GN      LTR OR TNFR OR TNFRSF3.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=LIVER;
RX      MEDLINE: 93252381.
RA      Baens M., Chaffain M., Cassiman J.J., den Bergh H., Marynen P.;
RT      "Construction and evaluation of a hmcDNA library of human l2p
RT      transcribed sequences derived from a somatic cell hybrid.";
RL      Genomics 16:214-218(1993).

```

[2]
RN FUNCTION: 94225209.
RA MEDLINE: 94225209.
RA Crowe P.D., van Arsdale T.L., Walter B.N., Ware C.F., Hession C.,
RA Ehrenfeld B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
RA "A lymphotoxin-beta-specific receptor."
RL Science 264:707-710(1994).
CC - FUNCTION: RECEPTOR FOR THE LYMPHOTOXIN-BETA. POSSIBLE FUNCTION IN
CC IMMUNE DEVELOPMENT.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL: L04270; AAA36757.1; -
CC DR HSSP: P25942; 1CDF.
CC DR DIM: 600979; -
CC DR INTERPRO: IPR001368; -
CC DR PROSITE: PS00652; TNFR_C6; 4.
CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE: PS00650; TNFR_NGFR_2; 3.
CC KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 30
CC FT CHAIN 31 435
CC FT DOMAIN 31 227
CC FT TRANSMEM 228 248
CC FT DOMAIN 249 435
CC FT DOMAIN 42 211
CC FT REPEAT 42 81
CC FT REPEAT 82 124
CC FT REPEAT 125 168
CC FT REPEAT 169 211
CC FT REPEAT 211 258
CC FT DISULFID 43 58
CC FT DISULFID 59 72
CC FT DISULFID 62 80
CC FT DISULFID 83 98
CC FT DISULFID 101 116
CC FT DISULFID 104 124
CC FT DISULFID 126 132
CC FT DISULFID 139 148
CC FT DISULFID 142 167
CC FT DISULFID 170 185
CC FT CARBOHYD 40 40
CC FT CARBOHYD 177 177
CC FT CARBOHYD 177 177
CC SO SEQUENCE 435 AA; 46709 MW; 62462656022F656F CRC64;
Query Match 11.2%; Score 244; DB 1; Length 435;
Best Local Similarity: 26.9%; Pred. No. 1.8e-10;
Matches 54; Conservative 32; Mismatches 93; Indels 22; Gaps 6;
QY 9 LVLVDIIETWTOETLPP-----KYLHYPETGHLQCDKCAPGYLKONCTVR 57
DB 18 VLGLFGLAASQFAVPVASENQTCDQKEYEPPG--HRICCSRPPTYSAKCSRI 75
QY 58 RKLVCPCPHSTSDSMHTSDCYVSPVCKELOSVAQ--ECNRTNHRVCECEGR--- 112
DB 76 RDTVCATCANSENHNNYLTICQLCRP--CDPVAGLEELAPCTSKRTQCCPGMECAA 134
QY 113 --LEIEFCLHRSCLPSPG--GVVAGTPEPRTVCKKCPDGFSGSTSKAPCIKHTNSTF 169
DB 135 WALECHCELLSCPPETELKDEVGKNNHVCPCAGHFOUNTSPSACQPHTRCENQ 194
QY 170 GLLLIOGNATHDNCVSGNRE 190
DB 195 GLVEAAPGTQSDTCKNPLE 215

RESULT 6
ID VT2_SFVKA STANDARD; PRT; 325 AA.
AC P25943;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN 12.
OS Shope fibroma virus (strain Kasza) (SFV).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
RN (1)
RN SEQUENCE FROM N.A.
RP MEDLINE: 87321103.
RA Upton C., Pelange A.M., McFadden G.;
RT "Tumorigenic poxviruses: genomic organization and DNA sequence of the
RT telomeric region of the Shope fibroma virus genome."
RL Virology 160:20-30(1987).
RN (2)
RN FUNCTION.
RP MEDLINE: 91207415.
RA Smith C.A., Davis T., Wignall J.M., Din W.S., Farrah T., Upton C.,
RA McFadden G., Goodwin R.G.;
RT T2 open reading frame from the Shope fibroma virus encodes a soluble
RT form of the TNF receptor."
RL Biochem. Biophys. Res. Commun. 176:335-342(1991).
CC - FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC REACH CELLULAR TARGET AND THEREBY DEAMPEINING THE POTENTIAL
CC ANTIVIRAL EFFECTS OF THE CYTOKINE.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC
CC EMBL: M17433; -; NOT ANNOTATED_CDS.
CC DR EMBL: A23727; CA01687.1; -
CC DR PIR: B43692; B43692.
CC DR HSSP: P19438; 1TNR.
CC DR INTERPRO: IPR001368; -
CC DR PEAM: PF00020; TNFR_C6; 2.
CC DR PROSITE: PS00652; TNFR_NGFR_1; 2.
CC DR PROSITE: PS00650; TNFR_NGFR_2; 1.
CC KW Receptor; Glycoprotein; Repeat; Signal.
CC FT SIGNAL 1 16
CC FT CHAIN 17 325
CC FT DOMAIN 27 186
CC FT REPEAT 27 62
CC FT REPEAT 63 104
CC FT REPEAT 105 147
CC FT REPEAT 148 186
CC FT CARBOHYD 105 105
CC FT CARBOHYD 181 181
CC FT CARBOHYD 205 205
CC FT CARBOHYD 238 238
CC FT CARBOHYD 238 238
CC SO SEQUENCE 325 AA; 35132 MW; 810530339198A71E CRC64;
Query Match 10.7%; Score 231.5; DB 1; Length 325;
Best Local Similarity 31.7%; Pred. No. 7e-10;
Matches 59; Conservative 19; Mismatches 91; Indels 17; Gaps 5;
QY 36 GHQ-----LLCDKADGYLYKHCHTVRRKTLVCPDHSYSDSMHTSDCYVSPVCKEL 90
DB 30 GHDYERKDGCCASCHBGFYASRLCGPSNWTVCSPCEDGTFFASTNHPACVACRCRGCGH 89
QY 91 QSVKQECNTHNRYVCECTPCRYLIEF-----FLKLRHSCPPGSGVVOAGTPEPRTVCKK 144

Db 90 LSESPQCDRHRDRCNOSTGNYCLLKNGNCRICAPQKPCAGVG-VSGHNRADDTLCEK 148
Qy 145 CPDGFSEGGSSKAPCIKHNKSTFGLLLIOGNATHDNCNGNREATQKCGIDVTL--- 201
Db 149 CPPTVSDLSPTBRCGTSFNYSVGFNLTPV-NETSCTTAGHNEVTKTEFTVTLNVT 207
Qy 202 -CEAF 206
Db 208 DCDPVE 213

RESULT 7
CD40_BOVIN STANDARD; PRT; 269 AA.
ID CD40_BOVIN STANDARD; PRT; 269 AA.
AC Q28203;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE CD40L RECEPTOR PRECURSOR (B-CELL SURFACE ANTIGEN CD40) (FRAGMENT).
GN TNFRSF5 OR CD40.
OC Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 97281252.
RA Hiranio A., Brown W.C., Estes D.M.;
RT "Cloning, expression and biological function of the bovine CD40
RT homologue: role in B-lymphocyte growth and differentiation in
RT cattle".
RL Immunology 90:294-300(1997).
CC - FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS CD40L.
CC - SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC EMBL; U57745; AAC48710.1; -
DR HSSP; P25942; 1CDF.
DR INTERPRO: IPR001368; -
DR PFAM; PF00020; TNFR_NGFR_1; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS50050; TNFR_NGFR_2; 1.
GN Receptor; B-cell; Glycoprotein; Transmembrane; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 >269 CD40L RECEPTOR.
FT DOMAIN 20 193 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 194 215 POTENTIAL.
FT DOMAIN 216 >269 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 25 187 4 X TNFR-CYS.
FT REPEAT 25 60 TNFR-CYS 1.
FT REPEAT 61 103 TNFR-CYS 2.
FT REPEAT 104 144 TNFR-CYS 3.
FT REPEAT 145 187 TNFR-CYS 4.
FT CARBOHYD 153 153 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 180 180 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT NON_TER 269 269
SQ SEQUENCE 269 AA; 29983 MM; 746903F30F95F387 CRC64;

Query Match 10.5%; Score 228; DB 1; Length 269;
Best Local Similarity 31.9%; Pred. No. 1.4e-09;
Matches 60; Conservative 21; Mismatches 89; Indels 18; Gaps 5;

29 LHYDPETG-----HQLLDCKAPGTYLKHQCTVRRKTLCPVCPDPSHYDTSWHTSDEC 80

Db 18 VHSPPATAGEKQYPPVNSLCLDLCPPGQKLVNDCTEVSKEGSCGGEPLSTWNEKCY 77
Qy 81 ---VYCSF-VKELQSVKQECNRTNHNVCCEBGRLL---EIFCLKHSNCPGSGVYA 133
Db 78 HENHYCNPNLGLRIOS---EGTLNTDITICVCEGOSHTECSCTPHSLCLGFGVKOI 134
Qy 134 GTPERNVCKKCPDGFPSGTSKAPCIKHNKSTFGLLLIOGNATHDNCNGNREATQ 193
Db 135 ATGLDITVCEPCPLGFSNVSAFCKHRTWTSCKRGVLVQHVGYNKTDVCCFQSMRT 194
Qy 194 KCGIDVTL 201
Db 195 LVYIPVTM 202

RESULT 8
VT2_MXYVL STANDARD; PRT; 326 AA.
ID VT2_MXYVL STANDARD; PRT; 326 AA.
AC P29825;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR PRECURSOR (PROTEIN T2).
GN T2.
OC Myxoma virus (strain Lausanne).
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91335768.
RA Upton C., Macen J.L., Schreiber M., McFadden G.;
RT "Myxoma virus expresses a secreted protein with homology to the tumor
RT necrosis factor receptor gene family that contributes to viral
RT virulence".
RL Virology 184:370-382(1991).
CC - FUNCTION: BINDS TO TNF-ALPHA AND BETA. PROBABLY PREVENTS TNF TO
CC ANTI-VIRAL EFFECTS OF THE CYTOKINE.
CC - SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
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CC EMBL; M95181; AAA46632.1; -
DR EMBL; A23726; CAA01688.1; -
DR PIR; A40566; GOVZML.
DR HSSP; P19438; ITNR.
DR INTERPRO: IPR001368; -
DR PFAM; PF00020; TNFR_NGFR_1; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
GN Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 326 TUMOR NECROSIS FACTOR SOLUBLE RECEPTOR.
FT DOMAIN 27 186 4 X TNFR-CYS.
FT REPEAT 27 62 TNFR-CYS 1.
FT REPEAT 63 104 TNFR-CYS 2.
FT REPEAT 105 147 TNFR-CYS 3.
FT REPEAT 148 186 TNFR-CYS 4.
FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 181 181 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 326 AA; 35208 MM; ABBF027E947292FF CRC64;

Query Match 10.1%; Score 220; DB 1; Length 326;

MD: MGI:104875; LTRR.
 DR INTERPRO: IPR001368; .
 DR PFM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 KW Receptor; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30
 FT CHAIN 31 415
 FT DOMAIN 31 223
 FT TRANSSEM 224 244
 FT DOMAIN 245 415
 FT DOMAIN 42 213
 FT REPEAT 42 81
 FT REPEAT 82 124
 FT REPEAT 125 170
 FT REPEAT 171 213
 FT DISULFID 43 58
 FT DISULFID 59 72
 FT DISULFID 62 80
 FT DISULFID 83 98
 FT DISULFID 101 116
 FT DISULFID 104 124
 FT DISULFID 126 132
 FT DISULFID 139 150
 FT DISULFID 142 169
 FT DISULFID 172 187
 FT CARBOHYD 40 40
 FT CARBOHYD 179 179
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A56AEF661 CRC64;

Query Match 9.5%; Score 206; DB 1; Length 415;
 Best Local Similarity 26.1%; Pred. No. 8.5e-08;
 Matches 53; Conservative 32; Mismatches 94; Indels 24; Gaps 8;

QY 9 LVLVDIIEMTQETLPKRYL-----HYDPETHQLCDKCAPGTLYKQCTVR 57
 DB 18 LILGSLGLVASQPOLVPRYRIENQTCMDQKREYEPM--HDVCCSRCPGEVFAVCSRS 75
 QY 58 KRLICVPPDHSYDTSMTSDSCVYCSFYCKELQSVKQ--EENRHNHVCDEEER---Y 112
 DB 76 QDVCTKTPHNSYNHNMHLSTQCLCRP-CDIVLGFEEVAPCTSDRKAECRCQPMSCVY 134
 QY 113 LEIE--FELKRR--SCPPGS--GVQAGTPERTVCKCPDGFSESTSKAPCIKHTNCS 167
 DB 135 LDNECVHEERLVLCQGTAEVDEIMDIDVNCVPCPKPGHFTSSBRACOPHTICE 194
 QY 168 TFGLLLIQGNATHDNCVSGNRE 190
 DB 195 IOGLVEAPGTSYDITCKNPPE 217

RESULT 11
 NGFR_HUMAN STANDARD: PRT: 427 AA.
 ID NGFR_HUMAN P08138;
 AC P08138;
 DT 01-AUG-1988 (Rel. 08, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-NGFR) (P75 ICD).
 GN NGFR OR TNFRSF16.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 87051725.
 RA Johnson D., Lanahan A., Buck C.R., Sehgal A., Morjan C., Mercer E.,
 RA Botchwell M., Chao M.;
 RT "Expression and structure of the human NGF receptor";
 RL Cell 47:545-554(1986).
 RN [2]

RP SEQUENCE OF 1-22 FROM N.A.
 RX MEDLINE: 89069903.
 RA Sehgal A., Patel N., Chao M.;
 RT "A constitutive promoter directs expression of the nerve growth factor
 RT receptor gene";
 RL Mol. Cell. Biol. 8:3160-3167(1988).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC -----
 DR EMBL: M4764; AAB59544.1; .
 DR EMBL: M21621; AAA36363.1; .
 DR PIR: A25218; GQHUN.
 DR HSP: P07174; INGR.
 DR MIM: 162010; .
 DR INTERPRO: IPR000488; .
 DR INTERPRO: IPR001368; .
 DR PFM: PF00020; TNFR_C6; 4.
 DR PFM: PF00531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 4.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal.
 FT SIGNAL 1 28
 FT CHAIN 29 427
 FT DOMAIN 29 250
 FT TRANSSEM 251 272
 FT DOMAIN 273 427
 FT DOMAIN 31 189
 FT REPEAT 31 65
 FT REPEAT 66 107
 FT REPEAT 108 147
 FT REPEAT 148 189
 FT DOMAIN 344 421
 FT DISULFID 32 43
 FT DISULFID 44 57
 FT DISULFID 47 64
 FT DISULFID 67 83
 FT DISULFID 86 99
 FT DISULFID 89 107
 FT DISULFID 109 122
 FT DISULFID 125 138
 FT DISULFID 128 146
 FT DISULFID 149 164
 FT DISULFID 167 180
 FT DISULFID 170 188
 FT DOMAIN 197 248
 FT CARBOHYD 60 60
 SQ SEQUENCE 427 AA; 45183 MW; B09FA143FB3D625B CRC64;

Query Match 9.1%; Score 199; DB 1; Length 427;
 Best Local Similarity 31.7%; Pred. No. 2.8e-07;
 Matches 52; Conservative 25; Mismatches 71; Indels 16; Gaps 6;
 QY 9 LVLVDIIEMTQETLPKRYLHYDPETHQLCDKCAPGTLYKQCTVRKRLICVPPDHS 68
 DB 17 LILGSLGLGAKKACAPGTLYTHSGE-----CKRKNLGEVAPPCA-NQTVCEPCIDS 70

OY 69 -SYTDSMHTSDECVYSPVCKELQSVKQECNRTNHNRYCECEGRYLE-----IEFCLAKR 122
 DB 71 VTFSDVVAATEPCKPCTE-CVGLQSMAPCEVADAVCAVGYODETGCAC---R 126
 OY 123 SCPPGSGVQAGTPERNYVCKCPDGFSGETSSKACICHTNC 166
 DB 127 VCRAGSGLVFSCODKONTVCEBCPDGTYSDANHVDPCLPCTVC 170
 RESULT 12
 NGFR_RAT ID STANDARD: PRT: 425 AA.
 AC P07174;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DT LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 (GP80-LNGFR) (P75 ICD).
 NGFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RN SEQUENCE FROM N.A.
 RX MEDLINE: 87115859.
 RA Radeke M.J., Misko T.P., Hsu C., Herzenberg L.A., Shooter E.M.;
 RT "Gene transfer and molecular cloning of the rat nerve growth factor
 RT receptor.";
 RT Nature 325:593-597(1987).
 RN [2]
 RN SEQUENCE OF 1-22 FROM N.A.
 RC TISSUE-LIVER;
 RX MEDLINE: 93077038.
 RA Metis M., Timusk T., Allikmets R., Saarna M., Persson H.;
 RT "Regulatory elements and transcriptional regulation by testosterone
 RT and retinoic acid of the rat nerve growth factor receptor promoter.";
 RT Gene 121:247-254(1992).
 RN [3]
 RN STRUCTURE BY NMR OF 334-418.
 RX MEDLINE: 97449145.
 RA Liepinsh E., Ilag L.L., Otting G., Ibanez C.F.;
 RT "NMR structure of the death domain of the p75 neurotrophin receptor.";
 RT EMBO J 16:4999-5005(1997).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PTM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 DR EMBL: X05137; CA28783.1.
 DR EMBL: X61269; NOT_ANNOTATED.CDS.
 DR PIR: A26431; A26431.
 DR PDB: INGR; 29-JUL-97.
 DR INTERPRO: IPR000488;
 DR INTERPRO: IPR001368;
 DR PFAM: PF000020; TNFR_C6; 4.
 DR PFAM: PF000531; death_1;
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS00500; TNFR_NGFR_2; 4.
 DR PROSITE: PS00017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;

KW Phosphorylation; Signal; 3D-structure.
 FT SIGNAL 1 29
 FT CHAIN 30 425
 FT DOMAIN 30 251
 FT TRANSMEM 252 273
 FT DOMAIN 274 425
 FT DOMAIN 32 190
 FT REPEAT 32 66
 FT REPEAT 67 108
 FT REPEAT 109 148
 FT REPEAT 149 190
 FT DOMAIN 198 249
 FT DOMAIN 354 419
 FT DISULFID 33 44
 FT DISULFID 45 58
 FT DISULFID 48 65
 FT DISULFID 68 84
 FT DISULFID 87 100
 FT DISULFID 90 108
 FT DISULFID 110 123
 FT DISULFID 126 139
 FT DISULFID 129 147
 FT DISULFID 150 165
 FT DISULFID 168 181
 FT DISULFID 171 189
 FT CARBOHYD 61 71
 FT CARBOHYD 71 61
 SQ SEQUENCE 425 AA; 45432 MW; B2E152D943827F8 CRC64;
 Query Match 9.1%; Score 197.5; DB 1; Length 425;
 Best Local Similarity 22.1%; Pred. No. 3.5e-07;
 Matches 95; Conservative 59; Mismatches 152; Indels 123; Gaps 19;

OY 9 LVLVLIIEHTQETLPRLYLNHPDPTGHLQCDKCAPGYLKQHCYVRRKTLVCPDHP 68
 DB 18 LVLILGVSSGAKETCTGLYTHSGE-----CKACNLDEGVAPCGA-NQYCEFCIDN 71
 OY 69 -SYTDSMHTSDECVYSPVCKELQSVKQECNRTNHNRYCECEGRYLEIE--FCLKHSRCP 125
 DB 72 VTFSDVVAATEPCKPCTE-CLGLQSMAPCEVADAVCAVGYODETGCACSVCH 130
 OY 126 PGSGVQAGTPERNYVCKCPDGFSGETSSKACICHTNCSIFGLLLQKGNATDNC 185
 DB 131 VGSGLVFSODKONTVCEBCPDGTYSDANHVDPCLPCTVCEDTEROL----- 178
 OY 186 SGNREATOKGIDVTLCCEAFRF-----AVPTK--IIPMLSYL 223
 DB 179 ---RECT--RADAE---CEELPGMIRSTPBGSDSTAFTQEPVPPEDOLVPSVADM 232
 OY 224 VDSLPTKVAVESVERIKRRHSSQE-----QTOLLKLMK--HONRDOE 265
 DB 233 VTFVVG-----SSQVYVIRGFTDNLIPVCSILAAVVVGLVAYIAFKRNSCKOKGA 286
 OY 266 MVAKTIQ-----DIDLCSSVQRHGHSHNLTEQLA---LMESLPCKK-- 306
 DB 287 NSRPVQCTPPEGEKLSHDSGISVDSOSLHDQFTQTASGALKGDGNLYSLPLTKRE 346
 OY 307 -----ISPEIER--TRKCKSSEOLKTLKLRINKGDOD--TLKG 344
 DB 347 EYVKLNGDTWRHLAGELGYQPEHIDFTHEAC---PYRALLASH---GAQDSATLDA 398
 OY 345 LMYALKHKK 353
 DB 399 LLAALRRIQ 407
 RESULT 13
 FASA_BOVIN STANDARD: PRT: 323 AA.
 ID FASA_BOVIN
 AC P51867;
 DT 01-OCT-1996 (Rel. 34, Created)

DT 01-OCT-1996 (Rel. 34, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
 DE (APO-1 ANTIGEN) (CD95).
 GN TNFRSF6 OR APT1 OR FAS.
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 CC Bovidae; Bovinae; Bos.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE; 96226401.
 RA Yoo J., Stone R.T., Beattie C.W.;
 RT "Cloning and characterization of the bovine Fas.",
 RL DNA Cell Biol. 15:227-234(1996).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
 CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
 CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
 CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
 CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
 CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
 CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
 CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
 CC SUICIDE OF MATURE T-CELLS, OR BOTH (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
 CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
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 CC
 CC EMBL: U34794; AAC48546.1; -
 CC HSP: P25445; IDPF.
 DR INTERPRO: IPR000488; -
 DR INTERPRO: IPR001368; -
 DR PFM: PF000531; death; 1.
 DR PFM: PF000531; death; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; 2.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal.
 FT SIGNAL 1
 FT CHAIN 17 323
 FT DOMAIN 17 170
 FT TRANSMEM 171 188
 FT TRANSSEM 189 323
 FT DOMAIN 189 323
 FT DOMAIN 45 163
 FT REPEAT 45 80
 FT REPEAT 81 124
 FT REPEAT 125 163
 FT REPEAT 163 306
 FT DOMAIN 238 306
 FT SEQUENCE 323 AA; 36445 MW; 4D88A903E9E1F4892 CRC64;

Query Match 8.7%; Score 190.5; DB 1; Length 323;
 Best Local Similarity 25.6%; Pred. No. 8.1e-07;
 Matches 77; Conservative 37; Mismatches 108; Indels 79; Gaps 18;

DB 37 HQLADKCAPETYLKQHCYVRKRT-LCYPCPD-HSYDTSWHTSDEVCYSPVCKELQ--S 92
 DB 53 HOFCCOPCPKRRKNGDCKRDGTPCEVLCSEGEYETDKSHSDKICRS-ICDEHGLE 111
 DB 93 VKQSCNFRHNVCCEBRYLEIEFCLKHSRCPGS-----GVVQAGTERTYVCKKCDG 148
 DB 112 VEONCTRTNRKCKRSNFCNSSPC---EHCNPTCTGHEGIIIEKCPJTNTCKK----- 163

QY 149 FFSGETSKAPCIKHTNCSFGLLI-----QKGNATHD--NVSGNREAT 192
 DB 164 ---GSR-----HAN-SLMALLIDPIVLIYYKVRERKKNNDYCNASANDNR 212
 QY 193 QKCIDVTLCEAEFAFPKTIIPMLSYVDSLPGTK---VNAESVERIK----- 241
 DB 213 QLNLTVDVL-----GKYIPS---IAEQRITEVEKFEVRKNGMEAKIDIDIMHD 257
 QY 242 RRHSSQCTPOLKLM--KNQND-----QEWKTIORI-DLCESSYGRHGHSLTT 292
 DB 258 NVHETAEQKVLNRNMYOSHGKNAVCTLTSLPKALAEKIDIVMDITNERENANLN 317
 QY 293 E 293
 DB 318 E 318
 RESULT 14
 ID NGFR_CHICK STANDARD; PRT; 416 AA.
 AC P18519;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, last sequence update)
 DT 01-OCT-2000 (Rel. 40, last annotation update)
 DE LOW-AFFINITY NERVE GROWTH FACTOR RECEPTOR PRECURSOR (NGF RECEPTOR)
 DE (GP80-LNGFR) (P75 ICD).
 GN NGFR.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE; 90166579.
 RA Large T.H., Weskamp G., Helder J.C., Radeke M.J., Misko T.P.,
 RA Shooter E.M., Reichardt L.F.;
 RT "Structure and developmental expression of the nerve growth factor
 RT receptor in the chicken central nervous system.",
 RL Neuron 2:1123-1134(1989).
 RN [2]
 RP SEQUENCE OF 21-416 FROM N.A.
 RX MEDLINE; 90152140.
 RA Heuer J.G., Fatemie-Najini S., Wheeler E.F., Bothwell M.;
 RT "Structure and developmental expression of the chicken NGF receptor.",
 RL Dev. Biol. 137:287-304(1990).
 CC -1- FUNCTION: LOW AFFINITY RECEPTOR WHICH CAN BIND TO NGF, BDNF,
 CC NT-3, AND NT-4.
 CC -1- SUBUNIT: NGF RECEPTOR CAN FORM A HOMODIMER THROUGH DISULFIDE
 CC BOND FORMATION.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
 CC -1- PM: N- AND O-GLYCOSYLATED AND IS PHOSPHORYLATED ON SERINE.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC -1- SIMILARITY: CONTAINS 1 DEATH DOMAIN.
 CC PIR: J00006; J00006.
 DR PIR: A60504; A60504.
 DR HSP: P07174; INGR.
 DR INTERPRO: IPR000488; -
 DR INTERPRO: IPR001368; -
 DR PFM: PF000531; death; 4.
 DR PFM: PF000531; death; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 3.
 DR PROSITE: PS50050; TNFR_NGFR_2; 3.
 DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 KW Receptor; Neurogenesis; Transmembrane; Glycoprotein; Repeat;
 KW Phosphorylation; Signal.
 FT SIGNAL 1
 FT CHAIN 20 416
 FT DOMAIN 29 239
 FT TRANSEM 240 261
 FT DOMAIN 262 416
 FT DOMAIN 23 181

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FT REPEAT 23 57 TNFR-CYS 1.
FT REPEAT 58 100 TNFR-CYS 2.
FT REPEAT 101 140 TNFR-CYS 3.
FT REPEAT 141 181 TNFR-CYS 4.
FT DOMAIN 188 236 SER/THR-RICH.
FT DOMAIN 333 410 DEATH DOMAIN.
FT DISULFID 24 35 BY SIMILARITY.
FT DISULFID 36 49 BY SIMILARITY.
FT DISULFID 39 56 BY SIMILARITY.
FT DISULFID 59 75 BY SIMILARITY.
FT DISULFID 78 91 BY SIMILARITY.
FT DISULFID 81 99 BY SIMILARITY.
FT DISULFID 101 114 BY SIMILARITY.
FT DISULFID 117 130 BY SIMILARITY.
FT DISULFID 120 138 BY SIMILARITY.
FT DISULFID 141 156 BY SIMILARITY.
FT DISULFID 159 172 BY SIMILARITY.
FT DISULFID 162 180 BY SIMILARITY.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 36 36 C -> Y (IN REF. 2).
FT CONFLICT 173 173 T -> K (IN REF. 2).
FT CONFLICT 276 276 N -> S (IN REF. 2).
FT CONFLICT 396 396 K -> R (IN REF. 2).
SQ SEQUENCE 416 AA; 44654 MM; 68CEAAB54F4D2D56 CRC64;

Query Match 8.48; Score 184; DB 1; Length 416;
Best Local Similarity 30.98; Pred. No. 3.2e-06;
Matches 46; Conservative 28; Mismatches 67; Indels 8; Gaps 6;

OY 41 CDKAPGTYLHOGCTVRKRTLCVPPDH-SYTDWHTSDCEYCSFVCKELOSVOQECNR 99
DB 36 CKACNLGEGVQPCGV-NQTVCEPLDSVTSYSAPEKPCPTQ-CVGLHSMAPCPE 93
OY 100 TNHRYCECEBGRYLEIEF---CLKHRSCPPSGVQAGTPERNYCKKCPDGFSGETSS 156
DB 94 SDAVRCRCAYC-YFQDELDSGCKECSICEVGLGLFPCRDSDYTCESCEGTFDEANF 152
OY 157 KAPCIKHTNCTFGILLIQKGNATHDNVC 185
DB 153 VDPCLPCTICEE-NEVWKECTATSDAEC 180

RESULT 15
FASL_HUMAN STANDARD: PRT; 335 AA.
P25445;
01-MAY-1992 (Rel. 22, Created)
01-MAY-1992 (Rel. 22, Last sequence update)
01-OCT-2000 (Rel. 40, Last annotation update)
DE FASL RECEPTOR PRECURSOR (APOPTOSIS-MEDIATING SURFACE ANTIGEN FAS)
DE (APO-1 ANTIGEN) (CD95 ANTIGEN).
GN TNFRSF6 OR APT1 OR FAS OR FASL.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 91309137.
RA Itoh N., Yonehara S., Ishii A., Yonehara M., Mizushima S.I.,
RA Sameshima M., Hase A., Seto Y., Nagata S.;
RT "The polypeptide encoded by the cDNA for human cell surface antigen
RT Fas can mediate apoptosis."
RL Cell 66:233-243(1991).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 226-240; 269-291 AND 321-335.
RX MEDLINE; 92268122.
RA Oehm A., Behnmann I., Falk W., Pawlita M., Maier G., Klas C.,
RA Li-Weber M., Richards S., Dhein J., Trauth B.C., Ponstingl H.,
RA Krammer P.H.;
RT "Purification and molecular cloning of the Apo-1 cell surface
RT antigen, a member of the tumor necrosis factor/nerve growth factor
RT receptor superfamily. Sequence identity with the Fas antigen."

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RL J. Biol. Chem. 267:10709-10715(1992).
RN [3]
RP STRUCTURE BY: NMR OF 218-335.
RX MEDLINE; 97122332.
RA Huang B., Eberstadt M., Olejniczak E.T., Meadows R.P., Fesik S.M.;
RT "NMR structure and mutagenesis of the Fas (Apo-1/CD95) death domain."
RL Nature 384:638-641(1996).
CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS FASL. THE
CC ADAPTOR MOLECULE FADD RECRUITS CASPASE-8 TO THE ACTIVATED
CC RECEPTOR. THE RESULTING AGGREGATE CALLED THE DEATH-INDUCING
CC SIGNALING COMPLEX (DISC) PERFORMS CASPASE-8 PROTEOLYTIC
CC ACTIVATION. ACTIVE CASPASE-8 INITIATES THE SUBSEQUENT CASCADE OF
CC CASPASES (ASPARTATE-SPECIFIC CYSTEINE PROTEASES) MEDIATING
CC APOPTOSIS. FAS-MEDIATED APOPTOSIS MAY HAVE A ROLE IN THE
CC INDUCTION OF PERIPHERAL TOLERANCE, IN THE ANTIGEN-STIMULATED
CC SUICIDE OF MATURE T-CELLS, OR BOTH.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- DOMAIN: CONTAINS A DEATH DOMAIN INVOLVED IN THE BINDING OF FADD,
CC AND MAYBE TO OTHER CYTOSOLIC ADAPTOR PROTEINS.
CC -1- SIMILARITY: CONTAINS A LA-NGR/TNFR-TYPE CYSTEINE-RICH REGION.
CC -1- DATABASE: NAME-PROV; NOTE-CD guide CD95 entry;
CC WWW-"HTTP://WWW.NCBI.NLM.NIH.GOV/PROV/CD/CD95.HTM".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.slb.ch/announce/
CC or send an email to license@slb.ch).
CC -----
DR EMBL; M67454; AAA63174.1; -
DR EMBL; X63717; CAA45250.1; -
DR PIR; A40036; A40036.
DR PIR; S24543; S24543.
DR PDB; 1DDF; 12-NOV-97.
DR MIM; 134637; -
DR INTERPRO; IPR000488; -
DR INTERPRO; IPR001368; -
DR PFAM; PF00020; TNFR_C6; 2.
DR PFAM; PF00531; death; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS50050; TNFR_NGFR_2; 2.
DR PROSITE; PS50017; DEATH_DOMAIN; 1.
DR KMW Apoptosis; Receptor; Glycoprotein; Transmembrane; Repeat; Signal;
RW 3D-structure.
FT SIGNAL 1 16
FT CHAIN 17 335
FT DOMAIN 17 173
FT TRANSSEM 174 190
FT TRANSSEM 191 335
FT DOMAIN 47 166
FT DOMAIN 47 83
FT REPEAT 84 127
FT REPEAT 84 127
FT REPEAT 128 166
FT REPEAT 128 166
FT DOMAIN 230 314
FT CARBOHYD 118 118
FT CARBOHYD 136 136
FT SEQUENCE 335 AA; 37732 MM; 0139942535111410 CRC64;

Query Match 8.48; Score 182; DB 1; Length 335;
Best Local Similarity 25.58; Pred. No. 3.4e-06;
Matches 76; Conservative 34; Mismatches 114; Indels 74; Gaps 15;

OY 19 TQOETLPKXHYHPYEPGHOLZCKACAPGYLKHCHCYR-RKTCVQCPD-HSTYDSMHT 76
DB 42 TTVFQNLGEGVQPCGV-NQTVCEPLDSVTSYSAPEKPCPTQ-CVGLHSMAPCPE 97
OY 77 SDEYCSFVCKELOSVOQECNR-TNHRVCECEBGRYLEIEFCLKHRSCPPSGGVQAG 134
DB 98 SSKRCRCR-LCDEGHGCTVQVINCRTIRONTKCRCPNFCNATVC---EHCDF----- 145

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:29 ; Search time 40.04 Seconds

(without alignments)
342,450 Million cell updates/sec

Title: US-09-389-545-2

Sequence: 1 MNKWLCCALLVLDITETTT.....OKLFLEMIGNOVSVKISCL 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Total number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_36:*

1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseq/AA1981.DAT:*

3: /SIDSL/gcgdata/geneseq/geneseq/AA1982.DAT:*

4: /SIDSL/gcgdata/geneseq/geneseq/AA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseq/AA1984.DAT:*

6: /SIDSL/gcgdata/geneseq/geneseq/AA1985.DAT:*

7: /SIDSL/gcgdata/geneseq/geneseq/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseq/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseq/AA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseq/AA1989.DAT:*

11: /SIDSL/gcgdata/geneseq/geneseq/AA1990.DAT:*

12: /SIDSL/gcgdata/geneseq/geneseq/AA1991.DAT:*

13: /SIDSL/gcgdata/geneseq/geneseq/AA1992.DAT:*

14: /SIDSL/gcgdata/geneseq/geneseq/AA1993.DAT:*

15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT:*

16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT:*

17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT:*

18: /SIDSL/gcgdata/geneseq/geneseq/AA1997.DAT:*

19: /SIDSL/gcgdata/geneseq/geneseq/AA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseq/AA1999.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2179	100.0	401	18	Mouse osteoprotegerin
2	2079	95.4	401	18	Rat osteoprotegerin
3	1900	87.2	401	20	Tumour necrosis fa
4	1900	87.2	401	20	Human FTHMA-070 pr
5	1900	87.2	401	20	Human FTHMA-070 pr
6	1895	87.0	401	17	Full length osteoc
7	1895	87.0	401	19	Human OCIF genome
8	1892	86.8	401	18	Human osteoprotege
9	1892	86.8	401	21	Osteoprotegerin pro
10	1891	86.8	401	19	TR1 receptor prote
11	1885	86.5	401	17	Mutated OCIF, OCIF
12	1885	86.5	401	17	Mutated OCIF, OCIF

13	1882	86.4	399	17	R99942
14	1880	86.3	401	17	R99934
15	1879	85.2	401	17	R99933
16	1875	86.0	401	17	R99935
17	1862.5	85.5	391	19	W53238
18	1852	85.0	395	19	Modified TR1 recep
19	1849	84.9	393	17	R99948
20	1828	83.9	380	17	R99924
21	1702.5	78.1	350	17	R99357
22	1670.5	76.7	350	17	R99936
23	1667	76.5	351	17	R99943
24	1645	75.5	359	17	R99939
25	1645	75.5	360	17	R99938
26	1620	74.3	359	17	R99937
27	1539	70.6	327	17	R99941
28	1510	69.3	321	17	R99949
29	1486.5	68.2	336	17	R99940
30	1481.5	68.0	349	20	W83928
31	1334	61.2	272	17	R99944
32	1096	50.3	420	20	W89224
33	1075.5	49.4	417	20	W89226
34	1073	49.2	208	20	W89231
35	1029	47.2	208	20	W89230
36	973	44.7	197	17	R99945
37	971.5	44.6	397	20	W89227
38	946	43.4	208	20	W89232
39	933	42.8	187	21	Y77464
40	928	42.6	187	17	R99950
41	810	37.2	366	20	W89228
42	709	32.5	143	17	R99946
43	666.5	30.6	145	17	R99930
44	665	30.5	154	17	R99929
45	536.5	24.6	311	20	W89229

ALIGNMENTS

RESULT 1	W83344	standard; Protein; 401 aa.
XX	W83344;	
AC	W83344;	
DT	20-Apr-1998	(first entry)
XX		
DE	Mouse osteoprotegerin.	
XX		
KW	Osteoprotegerin; antibody; diagnosis; affinity purification;	
KW	recombinant production; transgenic animal; treatment; prevention;	
KW	antisense oligonucleotide; probe; detection; screening; mouse;	
KW	bone disease; osteoporosis; Paget's disease; hypercalcaemia;	
KW	hyperparathyroidism; rheumatoid arthritis; osteomyelitis;	
KW	osteolytic metastasis; periodontal bone loss; bone necrosis;	
KW	osteopoenia; murine.	
XX		
OS	mus sp.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	90..1295
FT		/tag- a
FT		/product- osteoprotegerin
XX		
XX	DE19654610-A1.	
PN	26-JUN-1997.	
XX		
PD		
XX		
PF	20-DEC-1996;	96DE-1054610.
XX		
XX	03-SEP-1996;	96US-0706945.
PR	22-DEC-1995;	95US-0577788.
XX		
PA	(AMGE-) AMGEN INC.	

Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Human OCIF genome
Modified TR1 recep
Mutated OCIF, OCIF
Mature osteoclasto
Human tumour necro
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Mutated OCIF, OCIF
Human FTHMA-070 pa
Human FTHMA-070 pa
Tumour necrosis fa
Tumour necrosis fa
Tumour necrosis fa
Mouse osteoprotege
Rat osteoprotegeri
Mutated OCIF, OCIF
Tumour necrosis fa
Human osteoprotege
Primate protein se
Mutated OCIF, OCIF
Tumour necrosis fa
Mutated OCIF, OCIF
Osteoclastogenesis
Osteoclastogenesis
Tumour necrosis fa

Pt
XX Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
DR WPl: 1997-334271/31.
XX N-PSDB; T96062.
XX
PT Nucleic acid encoding osteoprotegerin - useful for treatment of
XX diseases involving excessive bone loss, e.g. osteoporosis
PS
Claim 23; Pages 106-107; 182pp; German.

xx
The present sequence is mouse osteoprotegerin (OPG). Anti-OPG
CC antibodies can be used in OPG diagnostic assays, and as affinity
CC purification materials. The OPG cDNA can be used to express
CC recombinant OPG and to generate transgenic animals. It can also
CC be used to regulate the level of OPG in mammals, specifically to
CC increase OPG levels, however the use of antisense sequences is
CC also contemplated. Fragments of the cDNA can be used as probes
CC to detect OPG expressing cells and tissue, and to screen cDNA
CC libraries for related sequences. OPG can be used to treat or
CC prevent bone diseases, specifically excessive bone loss, e.g.
CC osteoporosis, Paget's disease, hypercalcaemia,
CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC osteolytic metastases, periodontal bone loss, bone necrosis and
CC osteopenia.

Sequence 401 AA;

Query Match	100.0%	Score 2179;	DB 18;	Length	401;
Best Local Similarity	100.0%	Pred. N17;	2.1e-179;		
Matches 401; Conservative	0;	Mismatches	0;	Indels	0;
				Gaps	0

Oy	1	MNNELCGLLVLDLIDIEHTTQETLBPXYLIHNDRETHGOLICDCKAPETYLKONCTYARKT	60
Dd	1	mmkwccallvldldierltqetclpkylihdpeaqhqlldckapetylkphcvtvrik	60
Oy	61	LCVPCPDHSLYNDSMHTSDSECYVCSPPVCKELOLSVQOEONRTHNRYKCEDEEERYLEIEFCLK	120
Dd	61	lcvppdhslsyndsmhtsdsecyvspvckelolsvqoeonrthnrykceeeeryyleiefclk	120
Oy	121	HRSCEPDSGVVQACTPEERNVCKKCPDGFSGSETHSSKAPCIKHTNCTFGLLILOKGNAT	180
Dd	121	hrscepdsgvvqactpeernvckkcpgdfsgsethsskapihtnctfgllilokgnat	180
Oy	121	hrscepdsgvvqactpeernvckkcpgdfsfegesskapihkntcsftgllilqgnat	180
Oy	181	HDNWSGSRREATOKGCIQIVTLCSEAFPEEPANPTIINMILSVYDLSIPGRVNAESVERI	240
Dd	181	hdnwsgrreatokgcigivltlceeaftfayprckilpmlsvlydlsipgrkvnaesveri	240
Oy	241	KRRHSSQOEOTQOLKLMKHONRDDEMYKILIODIDLEESSVORHIGASNTTEQIALAME	300
Dd	241	krrhssqoeotqolklmkhonrdemvykiliodidleessvorhigasnntteqialame	300
Oy	301	SLPGKKISPEEIERTRKTCSSSEBOLKILSLMRKINGODQTLKGLMTALKHLKTSHEPKT	360
Dd	301	slpgkkispeeiertrktckssseqllkllslwrkngdqtlkglmyalkhlktshepkt	360
Oy	361	VTHSLRKTRMRLHSFTWRYLQXOLELHMGNOVSIVISCL	401
Dd	361	vthslrktrmrlhsftwrylyqxlflmlihgqvsvkiscsl	401

RESULT	2
W38343	
ID	W38343 standard; Protein; 401 AA.
XX	
XX	
AC	W38343;
XX	
DT	20-APR-1998 (first entry)
XX	
DE	Rat osteoprotegerin.
XX	
XX	
KN	Rat; osteoprotegerin; antibody; diagnosis; affinity purification.

KW	recombinant production; transgenic animal; treatment; prevention;
KW	antisense oligonucleotide; probe; detection; screening;
KW	bone disease; osteoporosis; Paget's disease; hypercalcaemia;
KW	hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
KW	osteolytic metastasis; periodontal bone loss; bone necrosis;
KW	osteopaenia.
OS	Rattus sp.
XX	
XX	DEL9654610-A1.
XX	
XX	26-JUN-1997.
XX	
XX	20-DEC-1996; 96DE-1054610.
XX	
XX	03-SEP-1996; 96US-0706945.
XX	
XX	22-DEC-1995; 95US-0577788.
XX	
XX	(AMGE-) AMGEN INC.
XX	
XX	Boyle WJ, Calzone FU, Lacey DL, Chang MS:
XX	
DR	WPI: 1997-334271/31.
DR	N-PSDB: T96061.
XX	
PT	Nucleic acid encoding osteoprotegerin - useful for treatment of
PT	diseases involving excessive bone loss, e.g. osteoporosis
PS	Claim 23; Pages 102-104; 182pp; German.
XX	
CC	The present sequence is rat osteoprotegerin (OPG). Anti-OPG
CC	antibodies can be used in OPG diagnostic assays, and as affinity
CC	purification materials. The OPG cDNA can be used to express
CC	recombinant OPG and to generate transgenic animals. It can also
CC	be used to regulate the level of OPG in mammals, specifically to
CC	increase OPG levels, however the use of antisense sequences is
CC	also contemplated. Fragments of the cDNA can be used as probes to
CC	detect OPG expressing cells and tissue, and to screen cDNA
CC	libraries for related sequences. OPG can be used to treat or
CC	prevent bone diseases, specifically excessive bone loss, e.g.
CC	osteoporosis, Paget's disease, hypercalcaemia,
CC	hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
CC	osteolytic metastases, periodontal bone loss, bone necrosis and
CC	osteopaenia.
XX	
XX	Sequence 401 AA:
XX	
XX	Query Match 95.4%; Score 2079; DB 18; Length 401;
XX	Best Local Similarity 94.5%; Pred. No. 8.5e-171;
XX	Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
QY	1 MNKWCALLVLDIIEWTQETLEPPKLYLHDPENGLDCKCAPGYLKOCHTVRRKT 60
DB	1 mkkwlcclllyfldliewtqetfppklylhydpetgrqlldckcapgyllkqhctvrrkt 60
QY	61 LCVPCPDHSYDWSHTSDEVCYCSFVCKELOSVKOEKRNTHRVCEBGRYLEFCIK 120
DB	61 lcvpcpdytsdswhtsdevcycsvckelqvkqecntrhvrcecegrylefcik 120
QY	121 HRSCEPDSGVVQACRPENNTYCKKRPDPFSGSESSKAPCIHTNCSIFGILLIOKNAT 180
DB	121 hrscepgpdyqvagrpentvckrkcpdpgffsgetaskapcrthncsslgilliqknat 180
QY	181 HDNWSGKREATOKGIVTLCSEAFEPFAVYTKRIIPWLSLVYVSLPGTKVNAESVERI 240
DB	181 hdnvsgnreatqncgldvtlceeffifaypcklpmwlslyvdsldgktnaesveri 240
QY	241 KRRHSSQDQFOLKIKMHONRDQEMVKRIIODIDLCESSVORHSHSLTTEQDLALME 300
DB	241 krrhssqdgqfqlklmwhqndqemvkkliqddldcessvgrhshsltteqdlrllme 300
QY	301 SLPGKKISPEIEIERTKTKCSSEQLKLILSLMRIKNGDQDILKGLMYLKHUKTSHFPKT 360

or T14 with a candidate compound in the presence of T1 or TR2; and (b) assessing the ability of the candidate compound to compete with T1 or TR2 binding to T12 or T14. TR and TR agonists and antagonists are useful for treating diseases caused by imbalance of IL or TR polypeptide levels, which cause: chronic and acute inflammation, arthritis, septicemia, autoimmune diseases, transplant rejection, graft vs. host disease, infection, stroke, ischemia, acute respiratory disease syndrome, restenosis, brain injury, AIDS, bone diseases, cancer, atherosclerosis and Alzheimer's disease. The present sequence represents a TNF-R related polypeptide T1.

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 20; Length 401;
Best Local Similarity 85.8%; Pred. No. 2.1e-155;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

1 MNKWLICALVLDI-1EMTQETLPKYLHYDEPGHQLCDKCAPGYLKQCTVARRK 59
1 mklilcca-lyfldislkwtqetfpylyhydeesthqlcdkcpptylkqhtakwk 59
60 TLVPCPDHSTDSWHTSDECVYCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119
60 tvcapcpdhytldswhtsdeclycspvckelqyvkgecnrthnvcceegryleiefcl 119
120 KHRSGPSSGVVAGTTPRRNVCCKCPDGFSGETSSKAPCKKHNCTFGLLQKQNA 179
120 khrcspgfigvvagtprrnvcckcpdgfsgetskcapckkhnctfglilqkqna 179
180 THDNVSGNREATORCGIDVTLCEAEFFRAVPTKIIIPNMLSVLSDSPGTVAESYER 239
180 thdnicsnsestqcgidvltlceaeaffravptkifpnmlsvlvdnlpgtkvaeseyer 239
240 IKRRHSSQEQTFOLIKMKHQRNDQEMVKIIOIDICESSVQRHGHNSITTEQLALM 299
240 ikrghsqeqtfqllkikwhqndqdvkkiiqididicessvqrhghnsltteqlslm 299
300 ESLPEKRTISPEIERTRKTKSSBOLKLSIMRIKNGDODTLGIMYALKHKLTSHPK 359
300 eslpkrtispeiertrtkssbolklslmrirkngdodtlgimalkhkltskthpk 359
360 TVTHSLKRTMRLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401
360 tvtsglkktrtirlhsftmyrlyoklflemignovsvkisl 401

RESULT 5
W83926 W83926 standard; Protein; 401 AA.
AC W83926;

01-MAR-1999 (first entry)
Human FTHMA-070 protein.

FTHMA-070: human; neurological disorder; therapy; diagnosis.

Key Location/Qualifiers
1..21
FT Peptide /label- Sig_peptide
FT Protein 22..401
FT /label- Mat_protein

W09848051-A2.
29-OCT-1998.
17-APR-1998; 98WO-US07714.

10-OCT-1997; 97US-0062017.
18-APR-1997; 97US-0044746.
(MTLL-) MILLENNIUM BIOTHERAPEUTICS INC.
Holtzman D, McCarthy SA;
MPI: 1999-024021/02.
N-PSDB: V69277.

New isolated human FTHMA-070 and T85 proteins - used to develop products for the diagnosis and therapy of disorders involving cellular processes, e.g. neuronal development.

Claim 8; Fig 1; 127pp; English.

This is the amino acid sequence of human FTHMA-070, a novel protein having homology to tumour necrosis factor receptor. The sequence was deduced from that of a cDNA clone (see V69277). Isolated from a cardiac coronary artery smooth muscle cell library. FTHMA-070 nucleic acids and polypeptides of the invention are useful as modulating agents in regulating a variety of cellular processes. They can be used for identifying compounds which bind to or modulate the activity of the polypeptides (claimed). They can also be used in screening assays, detection assays (e.g. chromosomal mapping, tissue typing, forensic biology), predictive medicine (e.g. diagnostic assays, prognostic assays, monitoring clinical trials, and pharmacogenomics), and methods of treatment (e.g. therapeutic and prophylactic) e.g. for neurological disorders.

Sequence 401 AA;

Query Match 87.2%; Score 1900; DB 20; Length 401;
Best Local Similarity 85.8%; Pred. No. 2.1e-155;
Matches 345; Conservative 26; Mismatches 29; Indels 2; Gaps 2;

1 MNKWLICALVLDI-1EMTQETLPKYLHYDEPGHQLCDKCAPGYLKQCTVARRK 59
1 mklilcca-lyfldislkwtqetfpylyhydeesthqlcdkcpptylkqhtakwk 59
60 TLVPCPDHSTDSWHTSDECVYCSPVCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119
60 tvcapcpdhytldswhtsdeclycspvckelqyvkgecnrthnvcceegryleiefcl 119
120 KHRSGPSSGVVAGTTPRRNVCCKCPDGFSGETSSKAPCKKHNCTFGLLQKQNA 179
120 khrcspgfigvvagtprrnvcckcpdgfsgetskcapckkhnctfglilqkqna 179
180 THDNVSGNREATORCGIDVTLCEAEFFRAVPTKIIIPNMLSVLSDSPGTVAESYER 239
180 thdnicsnsestqcgidvltlceaeaffravptkifpnmlsvlvdnlpgtkvaeseyer 239
240 IKRRHSSQEQTFOLIKMKHQRNDQEMVKIIOIDICESSVQRHGHNSITTEQLALM 299
240 ikrghsqeqtfqllkikwhqndqdvkkiiqididicessvqrhghnsltteqlslm 299
300 ESLPEKRTISPEIERTRKTKSSBOLKLSIMRIKNGDODTLGIMYALKHKLTSHPK 359
300 eslpkrtispeiertrtkssbolklslmrirkngdodtlgimalkhkltskthpk 359
360 TVTHSLKRTMRLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401
360 tvtsglkktrtirlhsftmyrlyoklflemignovsvkisl 401

RESULT 6
R99925 R99925 standard; Protein; 401 AA.
AC R99925;
DT 22-APR-1997 (first entry)

```

XX DE Full length osteoclastogenesis inhibitory factor.
XX XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX KW osteoporosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /note="Signal peptide"
XX FT 22..401
XX FT /note="Mature OCIF, claim 6"
XX PN MO9626217-A1.
XX PD 29-AUG-1996.
XX XX 20-FEB-1996; 96WO-JP00374.
XX PR 21-JUL-1995; 95JP-0207508.
XX PR 20-FEB-1995; 95JP-0054977.
XX XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX PI Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX DR WPI: 1996-402320/40.
XX DR N-PSDB: T36685.
XX PT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis.
XX PS Disclosure; Page 64-66; 183pp; Japanese.
XX XX
XX CC This sequence represents the full length osteoclastogenesis inhibitory
XX CC factor (OCIF) of the invention. The OCIF has a molecular weight by
XX CC SDS-PAGE of 60 kD under reducing conditions and 120 kD under non-
XX CC reducing conditions. The protein is adsorbed onto cation-exchangers
XX CC or heparin and its activity is lowered after 10 mins at 70 deg.C or
XX CC 30 mins at 56 deg.C, and is lost after 10 mins at 90 deg.C. OCIF is
XX CC useful in the control of bone resorption and therefore in the
XX CC treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX CC
XX Sequence 401 AA:

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Query Match 87.0%; Score 1895; DB 17; Length 401;
Best Local Similarity 85.6%; Pred. No. 5,6e-155;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
OY 1 MNMLCCALVLDI-IEWTTOETLPKYVHPETGHOILCDKCAPGTIKOHCYVRRK 59
DB 1 mnmlcca-ivfidistkwtgetfipkyihydeetshqilcdcpqgtylkqhtckwk 59
OY 60 TLVCPDHSYDTSWMTSDCVYCSYCKELQSVKQDCNTHNVCCEBGRYLEIEFCL 119
DB 60 tvcapcdphdydtswhstdeciyspyckelqyvkqdcntrhnceckegryleiefcl 119
OY 120 KHSRCPGSGVAGTPERTVCKKCPDGFSGFTSKACIKRTNSTGGLLQKGNM 179
DB 120 khscpbgfgyvqagperntvckrcpdpdgtfnsctskapcrkhtnsvtfgllltqkqna 179
OY 180 THNVCSGNREATQCGIDVTLCFAFFRAVPTKRIIPNLSVYVDSLPTKYNAESVER 239
DB 180 thnicsgnsesqkgidvtlceafrravptkriipnlsyvlvdilptknaesver 239
OY 240 IKRRHSSQEQFOLKLMKHONRQDEWVKRIIDIDLCSSVORHGLSHNLTEQLLMM 299
DB 240 lkrghssqeqftqlklmkhqnkdqdlvkkididlcensvqghghnaltfeqlslm 299

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OY 300 ESUHGKISPEIETRRKTCCKSEOLLKILSLMRKNGDPTLGLMAYALKHUKTSHPK 359
DB 300 es-pgkkygaedlekikackpsdqilklislvrlknqgdclkglmhalkhsckynfpr 359
OY 360 TVTHSLRKTWRFLHSFTMYRLYOKLFLEMIGNOVQSVKISCL 401
DB 360 tvtgsllktrflhsftmyklygkiflemignqvsvkisl 401

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RESULT 7
W53239
ID W53239 standard; Protein; 401 AA.
XX AC W53239;
XX XX 15-JUL-1998 (first entry)
XX DE Human OCIF genome DNA protein.
XX KW Human; OCIF; genome; osteoclast; antipyretic; osteoporosis;
XX KW rheumatism; multiple sclerosis.
XX OS Homo sapiens.
XX FH Key Location/Qualifiers
XX FT Peptide 1..21
XX FT Protein /label="signal"
XX FT 22..401
XX FT /label="OCIF_protein"
XX PN MO9807840-A1.
XX PD 26-FEB-1998.
XX PF 19-AUG-1997; 97WO-JP02859.
XX PR 19-AUG-1996; 96JP-0235928.
XX XX
XX PA (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX PI Morinaga T, Nakagawa N, Yasuda H;
XX DR WPI: 1998-169150/15.
XX DR N-PSDB: V20768.
XX PT Inhibition of osteoclast formation and/or antipyretic activity -
XX PT useful for, e.g. treating osteoporosis, rheumatism and multiple
XX PT sclerosis
XX PS Claim 4; Page 26-28; 36pp; English.
XX CC The present sequence represents human OCIF genome DNA protein which is
XX CC specifically claimed in the present invention. The present invention
XX CC describes: (1) a method of inhibiting the formation of osteoclasts
XX CC and/or antipyretic proteins, which have the following characteristics:
XX CC (i) MW determined by SDS-PAGE of approximately 60 kDa under reducing
XX CC conditions, and 60 kDa and 120 kDa under non-reducing conditions; (ii)
XX CC 401 aa sequence (111) (see W53239); (111). affinity to cation exchangers
XX CC and heparin; (iv) its osteoclast formation inhibiting activity reduced
XX CC by heating at 70 degrees Celsius for 10 minutes or 56 degrees Celsius
XX CC for 30 minutes, and (v) its antipyretic activity reduced by heating at
XX CC 90 degrees Celsius for 10 minutes, and (2) a method for preparing the
XX CC above proteins. The proteins are useful for, e.g. treatment and
XX CC prevention of osteoporosis, rheumatism or multiple sclerosis, and also
XX CC as antigens for immunological diagnosis of these diseases and disorders.
XX SO Sequence 401 AA:

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Query Match 87.0%; Score 1895; DB 19; Length 401;
Best Local Similarity 85.6%; Pred. No. 5,6e-155;
Matches 344; Conservative 25; Mismatches 30; Indels 2; Gaps 2;

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QY 1 MNKWLCCALVLDI-TEMTTOETLPKYLHYDEPETHOILCDKCAPGTLYKHQCTVRRK 59
 DB 1 mnlilcca-1vfidistkwetqetfppkylhydeetsqllcdkcpptylkqncakw 59
 QY TLVPCPDHSTYDSWMTSDCYVCSFYCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119
 DB 60 tvcapcdhytidswhsdeclcyspyckelqyvkgecnrtmrvceckegryleiefcl 119
 QY 120 KHNCSPPGSGVVOAGTPERTVCKKCPDGFSGSETSKAPCIKHTNCTSTGLLIQKNA 179
 DB 120 khrcspgfgvvgagtpertvckkcpdgffsnetsskpcrhtncsvglilltkgna 179
 QY 180 THDNVCSGNREATOKGIDVTLCEAEFFFAVPKTIIPNMLSVLSDLPKTVNAESVER 239
 DB 180 thdnicsgnesctqcgldvltlceaeaffrtavptkfcpmwlsvldnlpjtkvnaesver 239
 QY 240 IKRRHSSQEQTFOLLKLMKHONRDQEWKRIIDIDLCSSVORHLGHSNLTTEQLALM 299
 DB 240 ikrhssqeqtfqlklkwhqnkqgdvkkilqddicnsvgrhghnaltteqlrslm 299
 QY 300 ESLPGKATSPETIRTKTKSSQDLKLSLMRKINGDDOTLGLMALKHKTSHFPK 359
 DB 300 eslpgaktspeirtrtktkssqdlklslmrknkgddotlglmlalkshktyhfpk 359
 QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 DB 360 tvtslkrtrmrfshftmyrlyoklflemignovsvkisccl 401

RESULT 8
 ID W38345 standard: Protein; 401 AA.
 XX W38345;
 AC W38345;
 DX 20-APR-1998 (first entry)
 DE Human osteoprotegerin.
 XX
 KW Osteoprotegerin; antibody; diagnosis; affinity purification;
 KW recombinant production; transgenic animal; treatment; prevention;
 KW antisense oligonucleotide; probe; detection; screening; human;
 KW bone disease; osteoporosis; Paget's disease; hypercalcaemia;
 KW hyperparathyroidism; rheumatoid arthritis; osteomyelitis;
 KW osteolytic metastasis; periodontal bone loss; bone necrosis;
 KW osteopaenia.
 XX
 XX Homo sapiens.
 OS
 XX DE19654610-A1.
 PD 26-JUN-1997.
 XX
 XX 20-DEC-1996; 96DE-1054610.
 PF
 XX 03-SEP-1996; 96US-0706945.
 PR 22-DEC-1995; 95US-0577788.
 XX
 XX (AMGE-) AMGEN INC.
 PA Boyle WJ, Calzone FJ, Lacey DL, Chang MS;
 PI WPI; 1997-334271/31.
 XX N-PSDB; T96063.
 DR
 XX Nucleic acid encoding osteoprotegerin - useful for treatment of
 PT diseases involving excessive bone loss, e.g. osteoporosis
 XX
 PS Claim 23; Pages 109-111; 182pp; German.
 CC The present sequence is human osteoprotegerin (OPG). Anti-OPG
 CC antibodies can be used in OPG diagnostic assays, and as affinity
 CC purification materials. The OPG cDNA can be used to express

CC recombinant OPG and to generate transgenic animals. It can also
 CC be used to regulate the level of OPG in mammals, specifically to
 CC increase OPG levels, however the use of antisense sequences is
 CC also contemplated. Fragments of the cDNA can be used as probes to
 CC detect OPG expressing cells and tissue, and to screen cDNA
 CC libraries for related sequences. OPG can be used to treat or
 CC prevent bone diseases, specifically excessive bone loss, e.g.
 CC osteoporosis, Paget's disease, hypercalcaemia,
 CC hyperparathyroidism, rheumatoid arthritis, osteomyelitis,
 CC osteolytic metastases, periodontal bone loss, bone necrosis and
 CC osteopaenia.
 XX
 XX Sequence 401 AA;
 SQ
 Query Match 86.8%; Score 1892; DB 18; Length 401;
 Best Local Similarity 85.6%; Pred. No. 1e-154;
 Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
 QY 1 MNKWLCCALVLDI-TEMTTOETLPKYLHYDEPETHOILCDKCAPGTLYKHQCTVRRK 59
 DB 1 mnlilcca-1vfidistkwetqetfppkylhydeetsqllcdkcpptylkqncakw 59
 QY TLVPCPDHSTYDSWMTSDCYVCSFYCKELQSVKQECNRTNHNVCCEEGRYLEIEFCL 119
 DB 60 tvcapcdhytidswhsdeclcyspyckelqyvkgecnrtmrvceckegryleiefcl 119
 QY 120 KHNCSPPGSGVVOAGTPERTVCKKCPDGFSGSETSKAPCIKHTNCTSTGLLIQKNA 179
 DB 120 khrcspgfgvvgagtpertvckkcpdgffsnetsskpcrhtncsvglilltkgna 179
 QY 180 THDNVCSGNREATOKGIDVTLCEAEFFFAVPKTIIPNMLSVLSDLPKTVNAESVER 239
 DB 180 thdnicsgnesctqcgldvltlceaeaffrtavptkfcpmwlsvldnlpjtkvnaesver 239
 QY 240 IKRRHSSQEQTFOLLKLMKHONRDQEWKRIIDIDLCSSVORHLGHSNLTTEQLALM 299
 DB 240 ikrhssqeqtfqlklkwhqnkqgdvkkilqddicnsvgrhghnaltteqlrslm 299
 QY 300 ESLPGKATSPETIRTKTKSSQDLKLSLMRKINGDDOTLGLMALKHKTSHFPK 359
 DB 300 eslpgaktspeirtrtktkssqdlklslmrknkgddotlglmlalkshktyhfpk 359
 QY 360 TVTSLKRTMRFLSHFTMYRLYOKLFLEMIGNOVSVKISCL 401
 DB 360 tvtslkrtrmrfshftmyrlyoklflemignovsvkisccl 401

RESULT 9
 ID Y43400 standard: Protein; 401 AA.
 XX Y43400;
 AC Y43400;
 DX 28-JAN-2000 (first entry)
 DE Osteoprotegerin protein sequence.
 XX
 KW Osteoprotegerin; OPG; human; cardiovascular disease; occlusion;
 KW calcification; blood vessel; atherosclerosis; medial calcific sclerosis;
 KW Monckeberg's arteriosclerosis; therapy.
 XX
 XX Homo sapiens.
 OS
 XX WO9533942-A1.
 PN 28-OCT-1999.
 PD
 XX 21-APR-1999; 99MO-US08793.
 PF
 XX 23-APR-1998; 98US-0064832.
 PR
 XX (AMGE-) AMGEN INC.

XX PI Simonet S, Sarosi I;
XX DR WPI: 2000-013182/01.
XX DR N-PSDB: 237254.
XX PT Treating and preventing cardiovascular diseases, especially
XX PT atherosclerosis and Monckeberg's arteriosclerosis -
XX PS
XX PS Claim 9; Page 37-39; 43pp; English.
CC This sequence represents the human osteoprotegerin (OPG). The invention
CC relates to a method of treating or preventing cardiovascular disease by
CC administering OPG. The method can be used to treat and prevent
CC cardiovascular diseases associated with occlusion and calcification of
CC blood vessels, especially atherosclerosis or Monckeberg's
CC arteriosclerosis, i.e. medial calcific sclerosis. Using OPG to treat or
CC prevent cardiovascular diseases provides an alternative to invasive
CC treatments. OPG can be used as a single therapeutic for prevention and
CC treatment of both osteoporosis and cardiovascular diseases.
CC
XX
XX
SQ Sequence 401 AA;

Query Match 86.8%; Score 1892; DB 21; Length 401;
Best Local Similarity 85.6%; Pred. No. 1e-154;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;

1 MNKKLCCALLVLDI-IEMTQETLPKYLHYDETHQOLCDKCAPGTLYKCHCTVRK 59
1 mkkllcca-lvldisltkwetqetlppkylhydeethqllcdkcapgtlylkchctakwk 59
60 TLCPVCPDHSYTDMSWHSDECVYCSPVCKELQSVKQECNRTNRYVCECEGRYLEIFCL 119
60 tlcpvcpdhsytdmswhsdecvycspvckelqsvkqecnrtnryvcecegryleifcl 119
60 tvcapcpdhytswhtsdeclvcsyckelqyvcnrtnryvcecegryleifcl 119
120 KHRSCPGSGVYVQAGTPERNVTCKKCPGFFSGESSKAPCKKHNCSTFGILLIQGNA 179
120 khrcspgsgvyvqagtpernvtckkcpdggffsnesskaptckhncsvfgilltqgna 179
120 khrcspgfyvvgagtpernvtckrcpddgffsnesskaptckhncsvfgilltqgna 179
180 THDNVCSGNREATOKCGIDVTLCEAFRFAVPKTIIPNMLSVLVDSLPGRKVAESVER 239
180 thdnvcsnreatkcgidvtlceafrrfapvktpiipnmlsvlvdsllpgrkvaesver 239
180 thdnicsnsestckgldvtlceafrrfapvktpiipnmlsvlvdsllpgrkvaesver 239
240 IKRRHSSQEQTFOLLKLMKHONRDOEWYKIIQDIDCESSVORHLGHSNLTTEQLALM 299
240 ikrrhssegeqtfllklmwhqbnkagdiivkklididlcensvgrhlghsnltteqlslm 299
300 ESLGCKRTSPREIERKTRCKSSSEQLLKLISLRKNGDOTLKLMAALAKHKTSHRPK 359
300 eslgckrtspreierktrckssseqlklislrkngdotlklmalakhktshrp 359
300 eslpqkkgvgaedleklackpsdqlklislrkngdgtlklghakhsctlyhpk 359
360 TVTSHLRKTRFSLHSFTMYRRLYOKLFLEMIGNOVOSKISCL 401
360 tvtslhrtktrfslhsftmyrlyoklflemignovoskisc 401
360 tvtsqsktrfslhsftmyrlyoklflemignovoskisc 401

RESULT 10
W57635
ID W57635 standard: Protein; 401 AA.
XX
XX AC W57635;
XX DT 27-AUG-1998 (first entry)
XX DE
XX DE TRI receptor protein.
XX TR1 receptor: tumour necrosis factor receptor-1; TNF-alpha; TNF-beta;
XX TR1 inhibitor: tumour growth; tumour necrosis; microorganism infection;
XX cellular differentiation stimulation; ionising radiation; septic shock;
XX anti-viral response; growth regulator; immune response; meningococemia;
XX autoimmune disease; apoptosis; inflammation; cachexia; cerebral malaria;
XX AIDS; therapy.

XX OS Homo sapiens.
XX PN WO9812344-A1.
XX PN 26-MAR-1998.
XX PF 18-SEP-1996; 96WO-US15003.
XX PR 18-SEP-1996; 96WO-US15003.
XX PA (HUMA-) HUMAN GENOME SCI INC.
XX PI Fleischmann RD, Greene JM, Ni J;
XX DR WPI: 1998-217278/19.
XX DR N-PSDB: V24486.
XX PT New isolated tumour necrosis factor receptor - useful for developing
XX PT products for treating, e.g. tumours, auto-immune disease(s), graft
XX PT rejection, apoptosis or inflammation
XX PS
XX PS Claim 13; Fig 1; 11pp; English.
CC This sequence is a tumour necrosis factor receptor-1 (TR1) receptor
CC of the invention. The DNA can be used to produce a recombinant host
CC cell by inserting it into a vector, which is then used to transfect the
CC host cell. The TR1 receptor can bind both TNF-alpha and TNF-beta. TR1
CC receptor agonists can be used for inhibition of tumour growth and
CC necrosis of tumours. They can also be used to stimulate cellular
CC differentiation, e.g. T cell, fibroblasts or haematopoietic cell
CC differentiation, may be used to augment TR1's role in the host's defence
CC against microorganisms and prevent related disease. The agonists may
CC also be used to protect against the deleterious effects of ionising
CC radiation produced during a course of radiotherapy, e.g. denaturation of
CC enzymes, lipid peroxidation or DNA damage. The agonists may further be
CC used to mediate an anti-viral response, to regulate growth, to mediate
CC the immune response and to treat immunodeficiencies related to diseases
CC such as HIV. Antagonists to the TR1 receptor may be used to treat
CC autoimmune diseases, e.g. graft versus host rejection and allograft
CC rejection, and T cell mediated autoimmune diseases. They may also be used
CC to prevent apoptosis. They may also be used to prevent cytotoxicity and
CC to treat septic shock, meningococemia, inflammation, bacterial
CC infections, cachexia, cerebral malaria or AIDS. The products can also be
CC used for diagnosing the above diseases.
CC
XX
XX
SQ Sequence 401 AA;

Query Match 86.8%; Score 1891; DB 19; Length 401;
Best Local Similarity 85.3%; Pred. No. 1.2e-154;
Matches 343; Conservative 27; Mismatches 30; Indels 2; Gaps 2;

1 MNKKLCCALLVLDI-IEMTQETLPKYLHYDETHQOLCDKCAPGTLYKCHCTVRK 59
1 mkkllcca-lvldisltkwetqetlppkylhydeethqllcdkcapgtlylkchctakwk 59
60 TLCPVCPDHSYTDMSWHSDECVYCSPVCKELQSVKQECNRTNRYVCECEGRYLEIFCL 119
60 tlcpvcpdhsytdmswhsdecvycspvckelqsvkqecnrtnryvcecegryleifcl 119
60 tvcapcpdhytswhtsdeclvcsyckelqyvcnrtnryvcecegryleifcl 119
120 KHRSCPGSGVYVQAGTPERNVTCKKCPDGGFFSGESSKAPCKKHNCSTFGILLIQGNA 179
120 khrcspgsgvyvqagtpernvtckkcpdggffsnesskaptckhncsvfgilltqgna 179
120 khrcspgfyvvgagtpernvtckrcpddgffsnesskaptckhncsvfgilltqgna 179
180 THDNVCSGNREATOKCGIDVTLCEAFRFAVPKTIIPNMLSVLVDSLPGRKVAESVER 239
180 thdnvcsnreatkcgidvtlceafrrfapvktpiipnmlsvlvdsllpgrkvaesver 239
180 thdnicsnsestckgldvtlceafrrfapvktpiipnmlsvlvdsllpgrkvaesver 239
240 IKRRHSSQEQTFOLLKLMKHONRDOEWYKIIQDIDCESSVORHLGHSNLTTEQLALM 299
240 ikrrhssegeqtfllklmwhqbnkagdiivkklididlcensvgrhlghsnltteqlslm 299

OY 300 ESLPGKKSPEIEERTKCKSSDOLKLLSLMRKNGDODTLGIMVALKHLSHPK 359
 Db 300 eslpqkxvgaedlektlckpsdqlklslwrlngdqdtklgmhalkhsktyhfk 359
 OY 360 TVTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401
 Db 360 tvtgsllktrflhsftmyklygklflemignqvsvkisc1 401

RESULT 11

R99932 ID R99932 standard; Protein; 401 AA.

AC R99932;

DT 22-APR-1997 (first entry)

DE Mutated OCIF, OCIF-C20S.

KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
 osteoporosis.

OS Synthetic.

Key Location/Qualifiers

FT Peptide 1..21 /note= "Signal peptide"

FT Protein 22..401 /note= "Mature OCIF-C20S"

FT Misc-difference 202 /label= C20S

XX WO9626217-A1.

XX 29-AUG-1996.

XX 20-FEB-1996; 96WO-JP00374.

XX 21-JUL-1995; 95JP-0207508.

XX 20-FEB-1995; 95JP-0054977.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

XX WPI: 1996-402320/40.

XX N-PSDB: T33162.

DNA encoding osteoclastogenesis inhibitory factor protein - useful
 for bone resorption control, esp. treatment of osteoporosis

PS Claim 32; Page 96-98; 183pp; Japanese.

XX This sequence represents a mutated version of the full length
 CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
 CC sequence represents OCIF-C20S in which the 20th Cys residue in the
 CC mature OCIF protein is substituted by Ser. The OCIF of the invention
 CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
 CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
 CC cation-exchangers or heparin and its activity is lowered after 10 mins
 CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
 CC deg.C. OCIF is useful in the control of bone resorption and therefore
 CC in the treatment and prevention of disorders of bone resorption, e.g.
 CC osteoporosis.

XX Sequence 401 AA;

Query Match 86.5%; Score 1885; DB 17; Length 401;

Best Local Similarity 85.3%; Pred. No. 4,1e-154;

Matches 343; Conservative 26; Mismatches 31; Indels 2; Gaps 2;

OY 1 MNKPLCALVLLDI-IEMTQETLPKYLHYDEPETHQLDCKCAPETYLKOHCTVARK 59
 Db 1 mnlplcca-lyfldslsvtwtgetlprkylhydeetsqlldckcpptylkqnotakw 59
 OY 60 TLVCPDPHSTYDSNHTSDDEVYCSVCKELQSVKQECNFRTHNRYCEBGRYLEIEFCL 119
 Db 60 tvcapcphhytldsvhtsdedclycspvckelqyvkecntrhnryceckegryleiefcl 119
 OY 120 KHRSCPGSGVQAGTPERNVCKKCPDGFSGENSSAKPCIKHNSTFCLLIQKNA 179
 Db 120 khrscppgfygvaqagtpernvckrcpdpqfsgenssakpcrkhnscvflilqkqna 179
 OY 180 THDNVCSGNREATOKGIDVTLCEAEFFRFVAPTKIIPNWSLVADSLPGTKVNAESVER 239
 Db 180 thdnlcsgnsestqcgldvltlseaeffrfvcpkfpnwslvldnlpjtkvnaesver 239
 OY 240 IKRRHSQDQTFOLIKMKHONRDQEMVKKIIOIDIDCESSVQRHLGNSLTTEQLALM 299
 Db 240 lkrhsqeqdtfqlklkwhqkddqivkklldidlcensvqrhlghnltteqlrslm 299
 OY 300 ESLPGKKSPEIEERTKCKSSDOLKLLSLMRKNGDODTLGIMVALKHLSHPK 359
 Db 300 eslpqkxvgaedlektlckpsdqlklslwrlngdqdtklgmhalkhsktyhfk 359
 OY 360 TVTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVSVKISCL 401
 Db 360 tvtgsllktrflhsftmyklygklflemignqvsvkisc1 401

RESULT 12

R99931 ID R99931 standard; Protein; 401 AA.

AC R99931;

DT 22-APR-1997 (first entry)

DE Mutated OCIF, OCIF-C19S.

KW Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
 osteoporosis.

OS Synthetic.

Key Location/Qualifiers

FT Peptide 1..21 /note= "Signal peptide"

FT Protein 22..401 /note= "Mature OCIF-C19S"

FT Misc-difference 195 /label= C19S

XX WO9626217-A1.

XX 29-AUG-1996.

XX 20-FEB-1996; 96WO-JP00374.

XX 21-JUL-1995; 95JP-0207508.

XX 20-FEB-1995; 95JP-0054977.

XX (SNOW) SNOW BRAND MILK PROD CO LTD.

XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
 PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;

XX WPI: 1996-402320/40.

XX N-PSDB: T33161.

DNA encoding osteoclastogenesis inhibitory factor protein - useful
 for bone resorption control, esp. treatment of osteoporosis

PS Claim 29; Page 94-96; 183pp; Japanese.


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DT 22-APR-1997 (first entry)
XX Mutated OCIF, OCIF-C22S.
XX Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX osteoporosis.
XX Synthetic.
XX OS
XX Key Location/Qualifiers
XX Key 1..21
XX Peptide /note= "Signal peptide"
XX Protein 22..401
XX /note= "Mature OCIF-C22S"
XX Misc-difference 277
XX /label= C22S
XX FT
XX PN
XX PD
XX WO9626217-A1.
XX 29-AUG-1996.
XX 20-FEB-1996; 96WO-JP00374.
XX 21-JUL-1995; 95JP-0207508.
XX 20-FEB-1995; 95JP-0054977.
XX (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX MPI: 1996-402320/40.
XX N-PSDB: T33164.
XX DR
XX DR
XX FT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis
XX PS
XX PS Claim 38; Page 100-102; 183pp; Japanese.
XX CC This sequence represents a mutated version of the full length
XX CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX CC sequence represents OCIF-C22S in which the 22nd Cys residue in the
XX CC mature OCIF protein is substituted by Ser. The OCIF of the invention
XX CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX CC cation-exchangers or heparin and its activity is lowered after 10 mins
XX CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX CC deg.C. OCIF is useful in the control of bone resorption and therefore
XX CC in the treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX CC
XX Sequence 401 AA:
XX
XX Query Match 86.3%; Score 1880; DB 17; Length 401;
XX Best Local Similarity 85.1%; Pred. No. 1..1e-153;
XX Matches 342; Conservative 26; Mismatches 32; Indels 2; Gaps 2;
XX
XX QY 1 MAMKWLCCALLVLDL-IENTTQETLPKLIHDPETGHLCDKCAPGYIKQHCIVRRK 59
XX DB 1 mmlilccal-ivldisikwtlqetfipkylhydeetshqllcdckppgyllqkhtakwk 59
XX QY 60 TLTCVCPDHSYDSDWHTSECVYCSFVCKELQSVQKQENRTNRRVCECEGRTIEFEL 119
XX DB 60 tvcacpdpdhydsdwhtseclvcsfvcckelqsvqkqenrtnrrvceceegrylelefel 119
XX QY 120 KHRSCPSPGSGVQAQTPERNYCKKCPDGFSGETSSKAPCIKHTKCSYFGLLLIQGNA 179
XX DB 120 khrcspspgsgvqaqtpernyckkcpdghfsgetsskcapckhtkncsfyglillqkqna 179
XX QY 180 YHDNVCSGNREATQKCGIDVTLCEAEFRFAVPTKIPMWSLVLDSPGTGVNAESVER 239
XX DB 180 thdnicsgnsesatqkcgldvtlceaeffravptkftpmwlsvldspgtkvnaesver 239

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QY 240 IRRHSOQETFOLEKLNHONROEMWKTIIDIDICSSVORHGHSLTFEQLALM 299
DB 240 lrrhssqeqtlqllklnhqnkdqdlvklldidicemsvgrhghsltfegqlslm 299
QY 300 ESLPGRKISPEIERTRTCKSSQDLKLISLWRKINQDODTLKGLMYALNHLKTSHPK 359
DB 300 eslpgrkivgaediektlkaskpsdqlnlslwlrlknqdgdtllkglmalnkskxyhpk 359
QY 360 TVTSHLRKTRMRFHSFTWRYLYOKLFLEMIGNOVSVKISCL 401
DB 360 tvtsglrrktrfhsftwrylyoklflemignvsvkiscsl 401
XX
XX RESULT 15
XX R99933 standard; Protein; 401 AA.
XX AC R99933;
XX XX
XX DT 22-APR-1997 (first entry)
XX Mutated OCIF, OCIF-C21S.
XX DE
XX DE Osteoclastogenesis inhibitory factor; OCIF; heparin; bone resorption;
XX KW osteoporosis.
XX OS
XX Synthetic.
XX XX
XX Key Location/Qualifiers
XX Key 1..21
XX Peptide /note= "Signal peptide"
XX Protein 22..401
XX /note= "Mature OCIF-C21S"
XX FT Misc-difference 277
XX FT /label= C21S
XX FT
XX FT
XX PN
XX PN WO9626217-A1.
XX PD 29-AUG-1996.
XX PD 20-FEB-1996; 96WO-JP00374.
XX PF 21-JUL-1995; 95JP-0207508.
XX PR 20-FEB-1995; 95JP-0054977.
XX PR (SNOW ) SNOW BRAND MILK PROD CO LTD.
XX PA
XX PA Goto M, Higashio K, Kobayashi F, Mochizuki S, Morinaga T;
XX PI Nakagawa N, Shima N, Tsuda E, Ueda M, Yano K, Yasuda H;
XX PI MPI: 1996-402320/40.
XX DR N-PSDB: T33163.
XX DR
XX FT DNA encoding osteoclastogenesis inhibitory factor protein - useful
XX PT for bone resorption control, esp. treatment of osteoporosis
XX PS
XX PS Claim 35; Page 98-100; 183pp; Japanese.
XX CC This sequence represents a mutated version of the full length
XX CC osteoclastogenesis inhibitory factor (OCIF) of the invention. This
XX CC sequence represents OCIF-C21S in which the 21st Cys residue in the
XX CC mature OCIF protein is substituted by Ser. The OCIF of the invention
XX CC has a molecular weight by SDS-PAGE of 60 kD under reducing conditions
XX CC and 120 kD under non-reducing conditions. The protein is adsorbed onto
XX CC cation-exchangers or heparin and its activity is lowered after 10 mins
XX CC at 70 deg.C or 30 mins at 56 deg.C, and is lost after 10 mins at 90
XX CC deg.C. OCIF is useful in the control of bone resorption and therefore
XX CC in the treatment and prevention of disorders of bone resorption, e.g.
XX CC osteoporosis.
XX CC
XX Sequence 401 AA:
XX
XX SQ

```


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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:51:29 ; Search time 27.53 Seconds
(without alignments)
244.142 Million cell updates/sec

Title: US-09-389-545-2

Perfect score: 2179
Sequence: 1 MNKMLCCALLVLDIIEWTT.....OKLFLEMIGNOVSKISCL 401

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Indexed: 164575 seqs, 16761186 residues

Total number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/2/1aa/6_COMB.pep:*
- 4: /cgn2_6/ptodata/2/1aa/PCRTUS_COMB.pep:*
- 5: /cgn2_6/ptodata/2/1aa/PCRTUS1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2179	100.0	401	3	US-08-974-022-4 Sequence 4, Appl1
2	2079	95.4	401	3	US-08-974-022-2 Sequence 2, Appl1
3	1892	86.8	401	3	US-08-974-022-6 Sequence 6, Appl1
4	424.5	19.5	300	2	US-08-974-796-2 Sequence 2, Appl1
5	382	17.5	70	3	US-08-974-022-41 Sequence 41, Appl1
6	314	14.4	227	3	US-08-974-022-48 Sequence 48, Appl1
7	312	14.3	461	1	US-08-385-229-2 Sequence 2, Appl1
8	312	14.3	461	2	US-08-650-000-2 Sequence 2, Appl1
9	312	14.3	461	5	5395760-2 Patent No. 5395760
10	312	14.3	474	2	US-08-650-000-4 Sequence 4, Appl1
11	312	14.3	474	5	5395760-4 Patent No. 5395760
12	312	14.3	486	1	US-08-243-010-1 Sequence 1, Appl1
13	312	14.3	518	1	US-08-385-229-4 Sequence 4, Appl1
14	301.5	13.8	655	3	US-08-959-382-2 Sequence 2, Appl1
15	297	13.6	163	2	US-08-219-237B-5 Sequence 5, Appl1
16	296.5	13.6	164	2	US-08-232-087A-9 Sequence 9, Appl1
17	279	12.8	48	3	US-08-974-022-43 Sequence 43, Appl1
18	270	12.4	197	3	US-08-974-022-49 Sequence 49, Appl1
19	268.5	12.3	625	3	US-08-996-139-15 Sequence 15, Appl1
20	266.5	12.2	616	3	US-08-996-139-4 Sequence 4, Appl1
21	265.5	12.2	651	3	US-08-996-139-6 Sequence 6, Appl1
22	253	11.6	591	2	US-08-996-139-2 Sequence 2, Appl1
23	250.5	11.5	162	2	US-08-219-237B-7 Sequence 7, Appl1
24	242.5	11.1	197	2	US-08-505-606-1 Sequence 1, Appl1
25	233.5	10.7	325	4	US-08-974-022-47 Sequence 2, Appl1
26	229.5	10.5	207	3	US-08-974-022-47 Sequence 47, Appl1
27	229.5	10.5	355	1	US-08-292-549-6 Sequence 6, Appl1
28	226	10.4	355	1	US-08-292-549-6 Sequence 6, Appl1

29	220	10.1	326	1	US-08-292-549-4	Sequence 4, Appl1
30	220	10.1	326	4	PCT-US91-02207-4	Sequence 4, Appl1
31	207	9.5	283	4	PCT-US96-12374-2	Sequence 2, Appl1
32	199	9.1	224	3	US-08-974-022-50	Sequence 50, Appl1
33	187.5	8.6	159	2	US-08-232-087A-11	Sequence 11, Appl1
34	187.5	8.6	159	2	US-08-219-237B-6	Sequence 6, Appl1
35	187	8.6	120	3	US-08-974-022-42	Sequence 42, Appl1
36	182	8.4	335	2	US-08-219-237B-2	Sequence 2, Appl1
37	182	8.4	335	2	US-08-409-338-1	Sequence 1, Appl1
38	182	8.4	335	4	PCT-US95-17083-2	Sequence 2, Appl1
39	179.5	8.2	314	1	US-08-444-231-19	Sequence 19, Appl1
40	179.5	8.2	314	1	US-08-152-443A-19	Sequence 19, Appl1
41	179.5	8.2	314	4	PCT-US95-17083-4	Sequence 4, Appl1
42	177	8.1	191	3	US-08-974-022-52	Sequence 52, Appl1
43	177	8.1	256	4	US-08-236-918A-6	Sequence 6, Appl1
44	177	8.1	256	4	PCT-US96-03965-2	Sequence 2, Appl1
45	170	7.8	186	1	US-08-089-458B-6	Sequence 6, Appl1

ALIGNMENTS

RESULT 1
US-08-974-022-4
; Sequence 4, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehaven Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974, 022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577, 788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-4
Query Match 100.0%; Score 2179; DB 3; Length 401;
Best Local Similarity 100.0%; Pred. No. 8.6e-196;
Matches 401; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MNKMLCCALLVLDIIEWTTQETLPKKYIHPDEPGHOLCKCAFGYTLKHCHVRRRT 60
DB 1 MNKMLCCALLVLDIIEWTTQETLPKKYIHPDEPGHOLCKCAFGYTLKHCHVRRRT 60
OY 61 LCVPCDHSYTDSSWHSIDPCVYCSPIVCKELQSVKQECNTHNRVCECEGRLEIEFLCK 120

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|||||
Db 61 LCVPCHSTYDMSHTSDSECVYCSVCKELQSVKQECNRTNHRVCECEBGRYLEIEPCLK 120
QY 121 HRSCEPSSGVVQAGTPEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
Db 121 HRSCEPSSGVVQAGTPEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
QY 181 HDNVCSSGNREATQKCGIDVTLCCEAFEFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
Db 181 HDNVCSSGNREATQKCGIDVTLCCEAFEFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
QY 241 KRRHSOQTFQOLKLMKHQNRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
Db 241 KRRHSOQTFQOLKLMKHQNRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
QY 301 SLPGKKSIPERIEERTKRTCKSSBQLKLSLMRIKNGDQDTLGLMALKHLKTSHPKPT 360
Db 301 SLPGKKSIPERIEERTKRTCKSSBQLKLSLMRIKNGDQDTLGLMALKHLKTSHPKPT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
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RESULT 2
US-08-974-022-2
; Sequence 2, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-2
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Query Match 95.4%; Score 2079; DB 3; Length 401;
Best Local Similarity 94.5%; Pred. No. 1.9e-186;
Matches 379; Conservative 10; Mismatches 12; Indels 0; Gaps 0;
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QY 61 LCVPCHSTYDMSHTSDSECVYCSVCKELQSVKQECNRTNHRVCECEBGRYLEIEPCLK 120
Db 61 LCVPCHSTYDMSHTSDSECVYCSVCKELQSVKQECNRTNHRVCECEBGRYLEIEPCLK 120
QY 121 HRSCEPSSGVVQAGTPEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
Db 121 HRSCEPSSGVVQAGTPEPRNTVCKKCPDGFSGETSSKAPCIKHTNCSTFGLLIQKGNAT 180
QY 181 HDNVCSSGNREATQKCGIDVTLCCEAFEFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
Db 181 HDNVCSSGNREATQKCGIDVTLCCEAFEFRAVPTKIIPNMLSVLYDSLPGTKVNAESVERI 240
QY 241 KRRHSOQTFQOLKLMKHQNRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
Db 241 KRRHSOQTFQOLKLMKHQNRDQEMVKIIOIDIDLCSSVORHLGHSNLTTEQLALME 300
QY 301 SLPGKKSIPERIEERTKRTCKSSBQLKLSLMRIKNGDQDTLGLMALKHLKTSHPKPT 360
Db 301 SLPGKKSIPERIEERTKRTCKSSBQLKLSLMRIKNGDQDTLGLMALKHLKTSHPKPT 360
QY 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
Db 361 VTHSLRKTMRFLHSFTMYRLYOKLFLEMIGNOVOSVKISCL 401
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RESULT 3
US-08-974-022-6
; Sequence 6, Application US/08974022
; Patent No. 6015938
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,022
; FILING DATE: 12-DEC-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-974-022-6
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Query Match 86.8%; Score 1892; DB 3; Length 401;
Best Local Similarity 85.6%; Pred. No. 5.8e-169;
Matches 344; Conservative 26; Mismatches 30; Indels 2; Gaps 2;
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Db 1 MNLLCA-LVFLDISKTQTEFFPKYLYHDEBETHQLLCDKCPGTYLKQCHTAKWK 59
Oy 60 TLCPVPCDHSYTDMSWHTSDCYVCSYCKELOSVCOCNFTNHNVCCEGREGYLEIFCL 119
Db 60 TVCAPCDHYTDSWHTSDCYVCSYCKELOSVCOCNFTNHNVCCEGREGYLEIFCL 119
Oy 120 KHSNCPGSGVQAGTERTVCKKCPDGFSSGTSKACIKRTNSTGILLIQGNA 179
Db 120 KHSNCPGSGVQAGTERTVCKKCPDGFSSGTSKACIKRTNSTGILLIQGNA 179
Oy 180 THNVCNREATORCIGDITLCEAFRRVAPTKIIPNMLSVLVDSLPCKVAEVSER 239
Db 180 THNVCNREATORCIGDITLCEAFRRVAPTKIIPNMLSVLVDSLPCKVAEVSER 239
Oy 240 IKRHSOEOFTOLLKLMKHQNRDOENKIIODIDCESSVORHLHSNLTQELLALM 299
Db 240 IKRHSOEOFTOLLKLMKHQNRDOENKIIODIDCESSVORHLHSNLTQELLALM 299
Oy 300 ESLPGKISPEIEFTKRTCKSSFOLLKLSMIRKNGDDTLKGLMALKHLSHPRK 359
Db 300 ESLPGKISPEIEFTKRTCKSSFOLLKLSMIRKNGDDTLKGLMALKHLSHPRK 359
Oy 360 TVTSLKRTMRFLHSFTMYRLYOKLFLEMIGNOVQYKISCL 401
Db 360 TVTSLKRTMRFLHSFTMYRLYOKLFLEMIGNOVQYKISCL 401

RESULT 4
US-08-794-796-2
Sequence 2, Application US/08794796
Patent No. 5885800
GENERAL INFORMATION:
APPLICANT: Emery, John
APPLICANT: Tan, KB
APPLICANT: Truneh, Alem
APPLICANT: Young, Peter
TITLE OF INVENTION: Tumor Necrosis Related Receptor.
TITLE OF INVENTION: TR4
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESS: Smithline Beecham Corporation
STREET: 709 Swedeland Road
CITY: King of Prussia
STATE: PA
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
- COMPUTER: IBM Compatible
- OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/794,796
FILING DATE: 04-FEB-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Han, William T
REGISTRATION NUMBER: 34,344
REFERENCE/DOCKET NUMBER: GH50000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5219
TELEFAX: 610-270-4026
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 300 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-794-796-2
Query Match 19.5%; Score 424.5; DB 2; Length 300;
Best Local Similarity 39.0%; Pred. No. 6e-32;
Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;
Oy 26 PKYLHDPETGHOLLCDKCAPGTIYLKQCHTVRRKTLCPVPCDHSYTDMSWHTSDCYVCS 85
Db 34 PTYPMWDAETGERLYVQAOCPPGTFFVQPCRRDPTTCGPDPHHYQFMWYLERCRVCNV 93
Oy 86 VCKELOSVCOCNFTNHNVCCEGREGYLEIFCLIKHSCPSGSGVQAGTERTVCKKC 145
Db 94 LCGEREERACATHNRACRCRTGFFAHAGFCLERHASCPSGAGVAPARPSQNTQCPC 153
Oy 146 PDGFFSGTSSKAPCIKRTNSTGILLIQGNATHDNV--CSGNREATORCIGDITL 202
Db 154 PCGFSASSSSBQCPHRCFTALGLALNVPSSSHDICTCTGFPPLSTRVGAEE--C 211
Oy 203 EEAFFRPAVTKIIPNMLSVLVDSL 227
Db 212 ERAVIDFAPQDISIKRLQRLQAL 236

RESULT 5
US-08-974-022-41
Sequence 41, Application US/08974022
Patent No. 6015938
GENERAL INFORMATION:
APPLICANT: Boyle, William J.
APPLICANT: Lacey, David L.
APPLICANT: Calzone, Frank J.
APPLICANT: Chang, Ming-Shi
TITLE OF INVENTION: OSTEOPROTEGERIN
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESS: Amgen Inc.
STREET: 1840 Dehavenland Drive
CITY: Thousand Oaks
STATE: California
COUNTRY: USA
ZIP: 91320-1789
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,022
FILING DATE: 12-DEC-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Witter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 70 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-022-41

Query Match 17.5%; Score 382; DB 3; Length 70;
Best Local Similarity 94.3%; Pred. No. 7.3e-29;
Matches 66; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Oy 8 ALVLDIIMETQETLPKYLHNDPETHQLLCDKCAPGTIYLKQCHTVRRKTLCPVPCD 67

Db 1 ALVFLDIEMTQETLPPK--YLHYDPETGH-----OLCDKCAPGYTLKOH 60

QY 68 HSYTDSWHTS 77
Db 61 YSYTDSWHTS 70

RESULT 6
US-08-974-022-48

; Sequence 48, Application US/08974022
; Patent No. 6015938

; GENERAL INFORMATION:

; APPLICANT: Boyle, William J.

; APPLICANT: Lacey, David L.

; APPLICANT: Calzone, Frank J.

; TITLE OF INVENTION: OSTEOPROTEGERIN

; NUMBER OF SEQUENCES: 53

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Amgen Inc.

; STREET: 1640 Dehavenland Drive

; CITY: Thousand Oaks

; STATE: California

; COUNTRY: USA

; ZIP: 91320-1789

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; FILING DATE: 12-DEC-1995

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/577,788

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Winter, Robert B.

; REFERENCE/DOCKET NUMBER: A-378

; INFORMATION FOR SEQ ID NO: 48:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 227 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-974-022-48

Query Match 14.4%; Score 314; DB 3; Length 227;

Best Local Similarity 34.7%; Pred. No. 8.7e-22;

Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALVFLDIEMTQETLPPK--YLHYDPETGH-----OLCDKCAPGYTLKOH 53

Db 9 ALAVGLEL--WAAAHALPAQVAFTPYAPBPSTCLRLREYDQTAOMCCSKSPGOHAKVF 66

QY 54 CTVRKRTLCVCPPHSHSTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCEEGEGRYL 113

Db 67 CTKTSIDVDCSDCEDSTYQLQNMWVPECLSCGSSDQVETQACTRQNRICTCRPGWYC 126

QY 114 EI-----EFLKHSRCPGSGVVOAGTPERTVCKKCPDGFSEGTSSKAPCIKHTNCS 167

Db 127 ALSKQEGRLCAPLKRCPGFGVARPGETSDVYCKPCAPGTFSTSTSDICRPHQJCN 186

QY 168 TFGLLIKGNATHDNVCS 186

Db 187 VVAI-----PGNASRDVACT 201

RESULT 7

US-08-385-229-2
; Sequence 2, Application US/08385229
; Patent No. 5605690

; GENERAL INFORMATION:

; APPLICANT: Jacobs, Cindy A.

; APPLICANT: Smith, Craig A.

; TITLE OF INVENTION: Method of Treating TNF-Dependent

; NUMBER OF SEQUENCES: 5

; CORRESPONDENCE ADDRESSES:

; ADDRESSEE: Immunex Corporation

; STREET: 51 University Street

; CITY: Seattle

; STATE: Washington

; COUNTRY: U.S.A.

; ZIP: 98101

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/385,229

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/07/946,236

; FILING DATE:

; ATTORNEY/AGENT INFORMATION:

; NAME: Wright, Christopher L.

; REGISTRATION NUMBER: 31,680

; REFERENCE/DOCKET NUMBER: 2503

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (206) 587-0430

; TELEFAX: (206) 587-0606

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 461 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; US-08-385-229-2

Query Match 14.3%; Score 312; DB 1; Length 461;

Best Local Similarity 34.7%; Pred. No. 3.6e-21;

Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALVFLDIEMTQETLPPK--YLHYDPETGH-----OLCDKCAPGYTLKOH 53

Db 9 ALAVGLEL--WAAAHALPAQVAFTPYAPBPSTCLRLREYDQTAOMCCSKSPGOHAKVF 66

QY 54 CTVRKRTLCVCPPHSHSTDSWHTSDECVYCSPVCKELQSVKQECNRTHNRVCEEGEGRYL 113

Db 67 CTKTSIDVDCSDCEDSTYQLQNMWVPECLSCGSSDQVETQACTRQNRICTCRPGWYC 126

QY 114 EI-----EFLKHSRCPGSGVVOAGTPERTVCKKCPDGFSEGTSSKAPCIKHTNCS 167

Db 127 ALSKQEGRLCAPLKRCPGFGVARPGETSDVYCKPCAPGTFSTSTSDICRPHQJCN 186

QY 168 TFGLLIKGNATHDNVCS 186

Db 187 VVAI-----PGNASRDVACT 201

RESULT 8

US-08-650-000-2

; Sequence 2, Application US/08650000

; Patent No. 5945397

; GENERAL INFORMATION:

; APPLICANT: Smith, Craig A.

; APPLICANT: Goodwin, Raymond G.

; APPLICANT: Beckmann, M. Patricia

TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:
APPLICATION NUMBER: US 403,241
FILING DATE: 05-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 405,370
FILING DATE: 11-SEP-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 421,417
FILING DATE: 13-OCT-1989
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 523,635
FILING DATE: 10-MAY-1990
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2501-D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 461 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
-08-650-000-2

Query Match 14.3%; Score 312; DB 2; Length 461;
Best Local Similarity 34.7%; Pred. No. 3.6e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALLVLDITLMTQETLPK--YLHYDPETGH-----QLLDCAPGTYLKH 53
DB 9 ALAVGLEL--WAAAHALPAQVAFTPYAPFGSTCRRLREYIDQTAQCCSCSPGQAKVF 66
QY 54 CTVRRTLCVPCPDHSTYDMSWHTSDECVYCSFYCKELQSVKQECNRTNHNVCCEEGRYL 113
DB 67 CTKTSDIVCDSCDSSTYTQIMNWPBELSGSRCSDDQVETQACTRONKICRPGWC 126
QY 114 EI-----ECLKHSRCPGSGVYQAGTPERNYCKKCPDGFSGGTSKAPCIKHTNCS 167
DB 127 ALSKQSGRCAPLRKCRGFGVARGPTESDYVCKPCAPGTFSSNTSSIDICRPHQICN 186
QY 168 TFGLLIÖKGNATHDNVCS 186
DB 187 VVAI-----PGNASMDAVCT 201

RESULT 9
5395760-2

Patent No. 5395760
APPLICANT: SMITH, CRAIG A.;GOODWIN, RAYMOND G.;BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 2
LENGTH: 461
5395760-2

Query Match 14.3%; Score 312; DB 5; Length 461;
Best Local Similarity 34.7%; Pred. No. 3.6e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

QY 8 ALLVLDITLMTQETLPK--YLHYDPETGH-----QLLDCAPGTYLKH 53
DB 9 ALAVGLEL--WAAAHALPAQVAFTPYAPFGSTCRRLREYIDQTAQCCSCSPGQAKVF 66
QY 54 CTVRRTLCVPCPDHSTYDMSWHTSDECVYCSFYCKELQSVKQECNRTNHNVCCEEGRYL 113
DB 67 CTKTSDIVCDSCDSSTYTQIMNWPBELSGSRCSDDQVETQACTRONKICRPGWC 126
QY 114 EI-----ECLKHSRCPGSGVYQAGTPERNYCKKCPDGFSGGTSKAPCIKHTNCS 167
DB 127 ALSKQSGRCAPLRKCRGFGVARGPTESDYVCKPCAPGTFSSNTSSIDICRPHQICN 186
QY 168 TFGLLIÖKGNATHDNVCS 186
DB 187 VVAI-----PGNASMDAVCT 201

RESULT 10
US-08-650-000-4
Sequence 4, Application US/08650000
Patent No. 5945397
GENERAL INFORMATION:
APPLICANT: Smith, Craig A.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Beckmann, M. Patricia
TITLE OF INVENTION: Tumor Necrosis Factor Receptors
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/650,000
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/468,453
FILING DATE:
APPLICATION NUMBER: US/08/038,765
FILING DATE:

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; APPLICATION NUMBER: US 403,241
; FILING DATE: 05-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 405,370
; FILING DATE: 11-SEP-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 421,417
; FILING DATE: 13-OCT-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 523,635
; FILING DATE: 10-MAY-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Wright, Christopher L.
; REGISTRATION NUMBER: 31,680
; REFERENCE/DOCKET NUMBER: 2501-D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; INFORMATION FOR SEQ ID NO. 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 474 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-650-000-4

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Query Match	14.3%	Score 312	DB 21	Length 474
Best Local Similarity	34.3%	Pred. No. 3.8e-21		
Matches 70	Conservative 22	Mismatches 84	Indels 28	Gaps 5

[illegible]

RESULT 11
5760-4
PATIENT NO. 5395760
APPLICANT: SMITH, CRAIG A.; GOODWIN, RAYMOND G.; BECKMANN,
M. PATRICIA
TITLE OF INVENTION: DNA ENCODING TUMOR NECROSIS FACTOR-a AND
B-RECEPTORS.
NUMBER OF SEQUENCES: 17
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/523,635
FILING DATE: 10-MAY-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 421,417
FILING DATE: 13-OCT-1989
APPLICATION NUMBER: 405,370
FILING DATE: 11-SEP-1989
APPLICATION NUMBER: 403,241
FILING DATE: 05-SEP-1989
SEQ ID NO: 4;
LENGTH: 474
5395760-4

Query Match	14.38;	Score 312;	DB 5;	Length 474;
Best Local Similarity	34.38;	Pred. No. 3.8e-21;		

	Matches	70;	Conservative	22;	Mismatches	84;	Indels	28;	Gaps	5.
OY	5	LOCALVLDLIEHTTQELPKYL--HYDEPTGH-----QLDCKAPGNY	49							
Dd	6	LWALVFEEQL--WATGHVPAAVVLPTRKPPGTGECQISOERYDKRAOMCCAKCPGGY	63							
OY	50	EKOCHTVRRKLTCVPCPHSYSDWSMTSECVYCSPVKELOSVAKOENRTHNRYCEEE	109							
Dd	64	VAFHFNKTSDYVCADOCBAESMYQTWNQNPFRCLSCSSCTTDQVEIRACTKQNRYVACBAA	123							
OY	110	GXYLELF-----CLKHRSCPSSGVQATPERNTYCKRCQPGFFGEGLSSARPCIK	162							
Dd	124	GYYCALKTHTSGSROOMRLSRKCGPFGVAASSPA PNGNLCAKCAPGETFSDTTSTIDVCFP	183							
OY	163	HYNCSFTGLLIQKNATHDNVCS	186							
Dd	184	HRICS-----ILAI PGNASTDAYCA	203							

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1  RESULT 12
2  US-08-243-010-1
3  ; Sequence 1, Application US/08243010
4  ; Patent No. 5639597
5  ;
6  ; GENERAL INFORMATION:
7  ; APPLICANT: Lauffer, Leander
8  ; APPLICANT: Zetlmeissel, Gerd
9  ; APPLICANT: Okendo, Patricia
10 ; TITLE OF INVENTION: Cell-free Receptor Binding Assays, The
11 ; TITLE OF INVENTION: Production and Use Thereof
12 ;
13 ; NUMBER OF SEQUENCES: 6
14 ;
15 ; CORRESPONDENCE ADDRESS:
16 ; ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
17 ; ADDRESSEE: Dunner
18 ; STREET: 1300 I Street, N.W.
19 ; CITY: Washington
20 ; STATE: D.C.
21 ;
22 ; COUNTRY: USA
23 ; ZIP: 20005-3315
24 ;
25 ; COMPUTER READABLE FORM:
26 ; MEDIUM TYPE: Floppy disk
27 ; COMPUTER: IBM PC compatible
28 ; OPERATING SYSTEM: PC-DOS/MS-DOS
29 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
30 ;
31 ; CURRENT APPLICATION DATA:
32 ; APPLICATION NUMBER: US/08/243,010
33 ; FILING DATE: 13-MAY-1994
34 ; CLASSIFICATION: 435
35 ;
36 ; PRIOR APPLICATION DATA:
37 ; APPLICATION NUMBER: US 07/798,564
38 ; FILING DATE: 26-NOV-1991
39 ; APPLICATION NUMBER: DE P 40 37 837.3
40 ; FILING DATE: 28-NOV-1990
41 ;
42 ; ATTORNEY/AGENT INFORMATION:
43 ; NAME: Einaudi, Carol P.
44 ; REGISTRATION NUMBER: 32,220
45 ; REFERENCE/DOCKET NUMBER: 02481-1132-00000
46 ; TELECOMMUNICATION INFORMATION:
47 ; TELEPHONE: 202-408-4000
48 ; TELEFAX: 202-408-4400
49 ;
50 ; INFORMATION FOR SEQ ID NO: 1:
51 ; SEQUENCE CHARACTERISTICS:
52 ; LENGTH: 486 amino acids
53 ; TYPE: amino acid
54 ; TOPOLOGY: linear
55 ;
56 ; MOLECULE TYPE: peptide
57 ;
58 ; US-08-243-010-1

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Query Match      14.3%, Score 312; DB 1; Length 486;
Best Local Similarity 34.7%; Pred. No. 3.9e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5
07      8 ALLVLDLIEHTTQETLPPK--YLYHDEPTGH-----QLDCKCAPGYLKH 53

```


Db 9 ALAVGLEL--WAAAHALPAQVAFTPIAPFEPSTCHLRKYITQOTACMCCSKSPGOHAYF 66
OY 54 CTVRKRLCYPCPDHSTYDTSWHTSDEVCYSPVCKELOSVOKECNRTNHRVCEEGRYL 113
Db 67 CTKTSDFVDCSDCEDSTYQLNMWVPECLSCGSRSSDQVEYQACRRENRICTCRPGWYC 126
OY 114 EI-----EFLKHSRCPGSGVVOAGTPEPRNTYCKKCPDGFSGETSARKAPCIKHNTCS 167
Db 127 ALSROEGRLCAPLRKCRPGGVARPGTETSDVYCKPCAPGTFSTNTSTDICRPHOICN 186
OY 168 TFGLLIOLKGNATHDNVCS 186
Db 187 VVAL-----PGNASMDAVCT 201

RESULT 13
US-08-385-229-4
Sequence 4, Application US/08385229
Patent No. 5605690

GENERAL INFORMATION:
APPLICANT: Jacobs, Cindy A.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Method of Treating TNF-Dependent
TITLE OF INVENTION: Inflammation Using Tumor Necrosis Factor Antagonists
NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: Washington
COUNTRY: U.S.A.
ZIP: 98101

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,229
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/946,236
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Wright, Christopher L.
REGISTRATION NUMBER: 31,680
REFERENCE/DOCKET NUMBER: 2503
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 587-0606

INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 518 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-385-229-4

Query Match 14.3%; Score 312; DB 1; Length 518;
Best Local Similarity 34.7%; Pred. No. 4.3e-21;
Matches 69; Conservative 19; Mismatches 85; Indels 26; Gaps 5;

OY 8 ALVLDIIEWTQETLPPK--YLHYDETH-----QLCDKCAPGYLKH 53
Db 38 ALAVGLEL--WAAAHALPAQVAFTPIAPFEPSTCHLRKYITQOTACMCCSKSPGOHAYF 95
OY 54 CTVRKRLCYPCPDHSTYDTSWHTSDEVCYSPVCKELOSVOKECNRTNHRVCEEGRYL 113
Db 96 CTKTSDFVDCSDCEDSTYQLNMWVPECLSCGSRSSDQVEYQACRRENRICTCRPGWYC 155

OY 114 EI-----EFLKHSRCPGSGVVOAGTPEPRNTYCKKCPDGFSGETSARKAPCIKHNTCS 167
Db 156 ALSROEGRLCAPLRKCRPGGVARPGTETSDVYCKPCAPGTFSTNTSTDICRPHOICN 215
OY 168 TFGLLIOLKGNATHDNVCS 186
Db 216 VVAL-----PGNASMDAVCT 230

RESULT 14
US-08-959-382-2
Sequence 2, Application US/08959382
Patent No. 6013476

GENERAL INFORMATION:
APPLICANT: DEEN, KEITH
APPLICANT: HURLE, MARK
APPLICANT: YOUNG, PETER
APPLICANT: TAN, K.B.
TITLE OF INVENTION: Tumor Necrosis Related Receptor,
TITLE OF INVENTION: TR7
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: RATNER & PRESTIA
STREET: P.O. BOX 980
CITY: VALLEY FORGE
STATE: PA
COUNTRY: USA
ZIP: 19482

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/959,382
FILING DATE: 28-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/041,796
FILING DATE: 02-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: PRESTIA, PAUL F.
REGISTRATION NUMBER: 23,031
REFERENCE/DOCKET NUMBER: GH-50017
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-407-0700
TELEFAX: 610-407-0701
TELEX: 846169

INFORMATION FOR SPO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 655 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-959-382-2

Query Match 13.8%; Score 301.5; DB 3; Length 655;
Best Local Similarity 29.0%; Pred. No. 5.7e-20;
Matches 91; Conservative 40; Mismatches 150; Indels 33; Gaps 7;

OY 10 LVLDIIEWTQETLPPK--YLHYDETH-----QLCDKCAPGYLKH 63
Db 30 LLLGLFSTTAAPEKASNLIGYRHVDATGVLTCDCRPAQTYVSEHCTMTSLWCS 89
OY 64 PCPDHSTYDTSWHTSDEVCYSPVCKELOSVOKECNRTNHRVCEEGRYLIEFLKHS 123
Db 90 SCPVGTETRENGEIKCHDSOPCPWPMIEKLPCALLTDEHCTCPPMFOSNATCAPHTV 149
OY 124 CPPSGVVOAGTPEPRNTYCKKCPDGFSGETSARKAPCIKHNTSFGLLIOLKGNATHDN 183
Db 150 CPVGVGRKKGTEDEYRQGCARGTSDVPSVSMCKAATIDLSQNLVYIKRGTKETDN 209

OY 184 VC-----SGNRENTQKCGIDVTLCERAFRRFAYPTK-IIPNMLSVLYDSLPKTVNAESVE 238
Db 210 VCGILPSPSSSTSPSPGTAIFPRPEMETHFVPSSTYPRGN-----STESNSASV 262
OY 229 RIKRHSSEOETFOLLKMKHON---RDQEMVKKIIDIIDICSSVQRHLGHSNLTTEQ 294
Db 263 RPKVLSSTIQEGIVP-----DNTSARKEEDVNTKIPMLQYVNHQGPNNH-----ILK 311
OY 295 LLALMESLPGRKIS 308
Db 312 LLPMEATGGERKS 325

RESULT 15
US-08-219-237B-5
; Sequence 5, Application US/08219237B
; Patent No. 5874546
; GENERAL INFORMATION:
; APPLICANT: NAGATA, Shigekazu
; APPLICANT: ITOH, Naoto
; APPLICANT: YONEHARA, Shin
; TITLE OF INVENTION: DNA Coding for Human Cell Surface Antigen
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: James W. Helliwege
; STREET: P.O. Box 2266 Eads Station
; CITY: Arlington
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/219,237B
; FILING DATE: 28-MAR-1994
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/872,129
; FILING DATE: 22-APR-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: James W. Helliwege
; REGISTRATION NUMBER: 28,808
; REFERENCE/DOCKET NUMBER: 516762
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 163 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-219-237B-5

Query Match 13.6%; Score 297; DB 2; Length 163;
Best Local Similarity 36.8%; Pred. No. 2.1e-20;
Matches 60; Conservative 17; Mismatches 74; Indels 12; Gaps 3;

OY 30 HDPPEGHOLLDKCAPGYTLKQHCVRKRTLCVPCPDHSYDMSWHTSDCYCSPVCKE 89
Db 7 YTDQTA--OMCCSKSPGQHAKEVFCIKTSDTVQDSCEDSTYTQLMNVPECLSCGRCD 64
OY 90 LOSVROECNRTNRYVCEEGRYLEI-----EFLKHSRCPGSGVQAGTPERNTYCK 143
Db 65 DQVETQACTREGRNRICTCPGYCALSKQEGRLCAPLKRCRPGFVARPGTETSDYVCK 124
OY 144 KCPDGFSETGSSKAPCIKHTNCSFTGILLIKGNATHDNVCS 186
Db 125 PCAPGTFSNTSTSDICRPHQICNVVAI-----PGNASMDAVCT 163

Search completed: December 27, 2000, 10:53:53
Job time: 144 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:52:40 ; Search time 60.82 Seconds
(without alignments)
615.637 Million cell updates/sec

Title: us-09-389-545-8

Sequence: 1 MDKTHRCPPAPAPLLGGPS.....QKGNATHDNCISNSESTOK 401

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Gapop 10.0 , Gapext 0.5

Searched: 297973 seqs, 93374136 residues

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database : SPTREMBL.14.*

1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp.invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.podent:*
12: sp.virus:*
13: sp.vertibrate:*
14: sp.unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1009	44.9	401	4 000300	000300 homo sapien
2	1008	44.9	372	4 090HP4	090HP4 homo sapien
3	888	39.5	401	11 008712	008712 mus musculu
4	875	39.0	401	11 008727	008727 rattus norv
5	824.5	36.7	437	11 09RI44	09RI44 mus musculu
6	433	19.3	300	4 095407	095407 mus sapien
7	405.5	18.1	302	13 09PUS0	09PUS0 salvelinus
8	332.5	14.8	459	11 062327	062327 mus musculu
9	331	14.7	439	4 016042	016042 homo sapien
10	327	14.6	482	11 088734	088734 mus musculu
11	287	12.8	655	4 075509	075509 homo sapien
12	276	12.3	384	4 09HP60	09HP60 homo sapien
13	272.5	12.1	684	13 090544	090544 ginglymosto
14	252.5	11.2	616	4 091606	091606 homo sapien
15	252.5	11.2	625	11 035305	035305 mus musculu
16	234.5	10.4	348	12 057103	057103 monkeypox v
17	233.5	10.4	349	12 057099	057099 monkeypox v
18	231.5	10.3	349	12 057291	057291 monkeypox v
19	231.5	10.3	349	12 057100	057100 monkeypox v

20	231.5	10.3	349	12 057101	057101 monkeypox v
21	231.5	10.3	349	12 057102	057102 monkeypox v
22	230.5	10.3	348	12 057277	057277 monkeypox v
23	230.5	10.3	348	12 057108	057108 monkeypox v
24	229	10.2	348	12 057112	057112 variola vir
25	229	10.2	348	12 085407	085407 variola vir
26	226.5	10.1	349	12 057284	057284 camelipox vl
27	226.5	10.1	349	12 057098	057098 camelipox vl
28	226	10.1	349	12 057110	057110 variola vir
29	226	10.1	349	12 057111	057111 variola vir
30	226	10.1	349	12 089118	089118 variola vir
31	226	10.1	349	12 089098	089098 variola vir
32	223	9.9	350	12 057116	057116 cowpox viru
33	222.5	9.9	349	12 057097	057097 camelipox vl
34	222.5	9.9	355	12 085308	085308 cowpox viru
35	221	9.8	349	12 057109	057109 variola vir
36	220.5	9.8	349	12 057305	057305 cowpox viru
37	217.5	9.7	326	12 057120	057120 cowpox viru
38	217.5	9.7	326	12 057122	057122 cowpox viru
39	217.5	9.7	351	12 073559	073559 cowpox viru
40	217.5	9.7	360	12 057118	057118 cowpox viru
41	216.5	9.6	351	12 057117	057117 cowpox viru
42	214.5	9.6	350	12 057123	057123 cowpox viru
43	212.5	9.5	347	12 057115	057115 cowpox viru
44	211.5	9.4	351	12 057121	057121 cowpox viru
45	209.5	9.3	283	4 092956	092956 homo sapien

ALIGNMENTS

RESULT 1

ID 000300 PRELIMINARY: PRT: 401 AA.

AC 000300; OS0236;

DT 01-JUL-1997 (TREMBLrel. 04, Created)

DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)

DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)

DE OSTEOCYTE-PECULIN PRECURSOR (OSTEOCYTOGENESIS INHIBITORY FACTOR)

DE (OCIF) (TUMOR NECROSIS FACTOR RECEPTOR SUPERFAMILY MEMBER 11B).

GN TNFRSF11B OR OPG OR OCIF.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

[1]

RP SEQUENCE FROM N.A.

RP TISSUE-KIDNEY.

RX MEDLINE: 97262071.

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luechly K., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.,

RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density."

RT Cell 89:309-319(1997).

[2]

RP SEQUENCE FROM N.A.

RP TISSUE-LUNG FIBROBLAST.

RX MEDLINE: 98151033.

RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goto M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.,

RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro."

RT Endocrinology 139:1329-1337(1998).

[3]

RP SEQUENCE FROM N.A.

RP TISSUE-PLACENTA.

RX MEDLINE: 98351569.

RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.,

"Cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.";
 RL Ent. J. Biochem. 254:685-691(1998).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGHEST LEVELS IN LUNG, HEART, KIDNEY, PLACENTA, THYROID, SPINAL CORD AND LIVER. ALSO DETECTED IN A NUMBER OF OTHER HEMATOPOIETIC AND IMMUNE ORGANS. NOT DETECTED IN THE PANCREAS OR PERIPHERAL BLOOD LYMPHOCYTES.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AB008822; BAA32076.1; -
 DR EMBL: AB008821; BAA32076.1; JOINED.
 EMBL: U94332; BAB53709.1; -
 HSP: P25942; ICDF.
 DR MIM: 602643; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 OSTEOPROTEGERIN.
 FT DOMAIN 23 183 4 X TNFR-CYS.
 FT REPEAT 23 63 TNFR-CYS 1.
 FT REPEAT 64 106 TNFR-CYS 2.
 FT REPEAT 107 143 TNFR-CYS 3.
 FT REPEAT 144 201 TNFR-CYS 4.
 FT DOMAIN 306 365 DEATH DOMAIN.
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 118 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT CARBOHYD 98 98 POTENTIAL.
 FT CARBOHYD 152 152 POTENTIAL.
 FT CARBOHYD 165 165 POTENTIAL.
 FT CARBOHYD 178 178 POTENTIAL.
 FT CARBOHYD 289 289 POTENTIAL.
 FT CONFLICT 263 263 A -> D (IN REF. 2 AND 3).
 SEQUENCE 401 AA; 45996 MW; EB42PA51C9D7C7IE CRC64;

Query Match 44.98; Score 1009; DB 4; Length 401;
 Best Local Similarity 99.48; Pred. No. 6.6e-80;
 Matches 173; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 228 KETPPRYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSWHTSDEC 287
 DB 21 QETPPRYLHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSWHTSDEC 80
 OY 288 LYCSVPKCELYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 347
 DB 81 LYCSVPKCELYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 140
 OY 348 VCKRCPDGFSENETSSKAPCKRHTNCSYFGLLLTQKGNATHDNCISGNSSESTOK 401
 DB 141 VCKRCPDGFSENETSSKAPCKRHTNCSYFGLLLTQKGNATHDNCISGNSSESTOK 194
 RESULT 2
 ID 09UHP4 PRELIMINARY; PRT; 372 AA.
 AC 09UHP4;
 DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, last sequence update)
 DT 01-JUN-2000 (TREMblrel. 14, last annotation update)
 DE OSTEOPROTEGERIN (FRAGMENT).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=PLACENTA;
 RA He 2.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
 RT "Cloning and Expression of Osteoprotegerin from Homo sapiens.";
 RL Sheng Wu Hua Hsueh Yu Sheng Wu Wu Li Hsueh Pao 31:680-684(1999).
 DR EMBL: AF134187; AAF20168.1; -
 DR INTERPRO: IPR001368; -
 DR PFAM: PF00020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 FT NON_TER 1
 SQ SEQUENCE 372 AA; 42758 MW; F02527A5CD01CCD3 CRC64;

Query Match 44.98; Score 1008; DB 4; Length 372;
 Best Local Similarity 100.0%; Pred. No. 7.4e-80;
 Matches 173; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 229 ETTPPKYLYHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSWHTSDECL 288
 DB 1 ETTPPKYLYHDEETSHOGLCDKCPGTYLKHOKCTAKKTYCACPDHYTDSWHTSDECL 60
 OY 289 YCSVPKCELYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 348
 DB 61 YCSVPKCELYVQECNRTNRYVCECKEGRYLEIEFLKHSRCPGPGVYVQAGTPERNV 120
 OY 349 CKRCPDGFSENETSSKAPCKRHTNCSYFGLLLTQKGNATHDNCISGNSSESTOK 401
 DB 121 CKRCPDGFSENETSSKAPCKRHTNCSYFGLLLTQKGNATHDNCISGNSSESTOK 173
 RESULT 3
 ID 008712 PRELIMINARY; PRT; 401 AA.
 AC 008712;
 DT 01-JUL-1997 (TREMblrel. 04, Created)
 DT 01-JUL-1997 (TREMblrel. 04, last sequence update)
 DT 01-MAY-2000 (TREMblrel. 13, last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR) (OCIF).
 GN TNFRSF11B OR OPB.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/C; TISSUE=KIDNEY;
 RX MEDLINE: 97263071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G., Darose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";
 RT Cell 89:309-319(1997).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/OLA AND NIH SWISS;
 RX MEDLINE: 98382527.
 RA Mizuno A., Murakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T., Higashio K.;
 RA "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF) gene and its expression in embryogenesis.";
 RT Gene 215:339-343(1998).

CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- TISSUE SPECIFICITY: EXPRESSED AT HIGH LEVELS IN LIVER, LUNG,
 CC BRAIN, HEART, KIDNEY, STOMACH, INTESTINE, SKIN, CALVARIA AND
 CC PLACENTA. NOT DETECTED IN SPLEEN.
 CC -1- DEVELOPMENTAL STAGE: IN THE EMBRYO, HIGH LEVELS ARE DETECTED AT
 CC DAY 7. AT DAY 11, EXPRESSION DECREASES AND THEN INCREASES FROM DAY
 CC 15 TO DAY 17.
 CC -1- SIMILARITY: CONTRAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 CC EMBL: U94331; AAB53708.1; -.
 CC EMBL: AB013898; BAA28269.1; -.
 CC EMBL: AB013903; BAA33388.1; -.
 CC EMBL: AB013899; BAA33388.1; JOINED.
 CC EMBL: AB013900; BAA33388.1; JOINED.
 CC EMBL: AB013901; BAA33388.1; JOINED.
 CC EMBL: AB013902; BAA33388.1; JOINED.
 CC HSSP: P25942; ICDF.
 CC MGD: MGI:109587; OPG.
 CC INTERPRO: IPR001368; -.
 CC DR INTERPRO: IPR001368; -.
 CC DR PFAM: PF00020; TNFR_C6; 3.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC DR PROSITE: PS50017; DEATH_DOMAIN; 1.
 CC DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 201
 FT REPEAT 23 63
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 165 178
 FT CARBOHYD 178 289
 FT CARBOHYD 289 365
 FT VARIANT 138 138
 FT VARIANT 161 161
 FT VARIANT 165 165
 FT VARIANT 288 288
 FT VARIANT 296 296
 FT SEQUENCE 401 AA: 45923 MW: CAA6102D3B312470 CRC64;
 Query Match 39.5%; Score 888; DB 11; Length 401;
 Best Local Similarity 86.8%; Pred. No. 2.2e-69;
 Matches 151; Conservative 8; Mismatches 15; Indels 0; Gaps 0;

OY 348 VKCRPDGFENSTSSKAPCRKHTNCSYFGLLLTOKGNATHDNICGNSSEKX 401
 DB 141 VKCRPDGFENSTSSKAPCRKHTNCSYFGLLLTOKGNATHDNICGNSSEKX 194
 RESULT 4
 ID 008727 PRELIMINARY; PRT; 401 AA.
 AC 008727;
 DT 01-JUL-1997 (TREMBLrel. 04, Created)
 DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
 DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE OSTEOPROTEGERIN PRECURSOR (OSTEOCLASTOGENESIS INHIBITORY FACTOR)
 DE (OCIF).
 GN TNFRSF11B OR OPG.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=INTESTINE;
 RX MEDLINE; 97262071.
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luehry R., Nguyen H.Q., Wooden S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Day E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RA "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density";
 RL Cell 89:309-319(1997).
 CC -1- FUNCTION: MAY REGULATE BONE RESORPTION BY BLOCKING TERMINAL STAGES
 CC OF OSTEOCLAST DIFFERENTIATION AND ALLOWING ACCUMULATION OF NEWLY
 CC SYNTHESIZED BONE AND CARTILAGE. MAY INHIBIT IN VITRO
 CC OSTEOCLASTOGENESIS BY INTERRUPTING CELL-TO-CELL SIGNALING BETWEEN
 CC STROMAL CELLS AND OSTEOCLAST PROGENITORS.
 CC -1- SUBUNIT: HOMODIMER (MAJOR FORM) AND MONOMER (MINOR FORM) (BY
 CC SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: EXTRACELLULAR.
 CC -1- SIMILARITY: CONTRAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION;
 CC EMBL: U94330; AAB53707.1; -.
 CC DR HSSP: P25942; ICDF.
 CC DR INTERPRO: IPR001368; -.
 CC DR PFAM: PF00020; TNFR_C6; 4.
 CC DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 CC DR PROSITE: PS50050; TNFR_NGFR_2; 2.
 CC KW Glycoprotein; Repeat; Cytokine; Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 401
 FT DOMAIN 23 201
 FT REPEAT 23 63
 FT REPEAT 64 106
 FT REPEAT 107 143
 FT REPEAT 144 201
 FT DOMAIN 306 365
 FT DISULFID 41 54
 FT DISULFID 44 62
 FT DISULFID 65 80
 FT DISULFID 83 97
 FT DISULFID 87 105
 FT DISULFID 118 142
 FT DISULFID 145 160
 FT CARBOHYD 98 165
 FT CARBOHYD 165 178
 FT CARBOHYD 178 289
 FT CARBOHYD 289 365
 FT SEQUENCE 401 AA: 46192 MW: FFC6A31F1D4E573A CRC64;
 Query Match 39.0%; Score 875; DB 11; Length 401;
 Best Local Similarity 85.5%; Pred. No. 2.9e-68;
 Matches 148; Conservative 10; Mismatches 15; Indels 0; Gaps 0;

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OY 228 KETPEPKYLYHDETSKOLDCNCPGTYLKOHCTAKMKTYCAPCPDHYTDSMHTSDEC 287
DB 21 QETPEPKYLYHDETSKOLDCNCPGTYLKOHCTAKMKTYCAPCPDHYTDSMHTSDEC 80
OY 288 LYSPVCKELOYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPEPRNT 347
DB 81 VYSPVCKELOYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPEPRNT 140
OY 348 VCKRCPDGFSSNETSSKAPCRKHTNCSVFGILLTQKGNATHDNCISGNSSTQ 400
DB 141 VCKRCPDGFSSNETSSKAPCRKHTNCSVFGILLTQKGNATHDNCISGNSSTQ 193

RESULT 5
OY 09RI4 PRELIMINARY; PRT; 437 AA.
AC 09RI4;
RT 01-MAY-2000 (TEMBLrel. 13, Created)
RT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
RT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE GAMMAL HEAVY CHAIN OF MAB (FRAGMENT).
OS Mus. musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RA Wilde K.G., Yu X., Ekramodoullah A.K.M., Misra S.;
RT "Cloning of cDNAs encoding for anti-white pine blister rust monoclonal
RT antibody (Mab 7, its light and heavy chains) and construction of a
RT single chain antibody (scFv).";
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF152372; AAD0243.1; -.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PFAM: PF00047; 1g; 4.
DR PROSITE: PS00290; IG_MHC; UNKNOWN_1.
FT NON_TER 1 437
FT NON_TER 1 437
SQ SEQUENCE 437 AA; 48142 MW; 5C3A7B33E7D697C CRC64;

Query Match
Best Local Similarity 36.7%; Score 824.5; DB 11; Length 437;
Matches 141; Conservative 43; Mismatches 35; Indels 5; Gaps 2;

OY 7 CPE--CPABELGSPVFLPEPKPKDTLMSRDEVTGVVVDVSHEDPEVKENNYDGV 64
DB 217 CKPICIVPEV---SSVFIFPKPKDVLITLTPKVCVVVDISKDDPEVQFSWFVDVE 273
OY 65 VHAATKPREEOXNSTRVNVSVLTVLHODWLNKGEKCKVSNKLPAPIEETISKAGOP 124
DB 274 VHAATQTPREEOXSTRVNSVSLPIMHODWLNKGEKCKVSNKLPAPIEETISKAGRP 333
OY 125 REPOVYTLPEPSRDELTKNVSILTVKGFYPSDIAVEMESGQENNYKTPPYLDSGS 184
DB 334 KAPQVYIIPPEKEMADKXSLTGMITDFREDITVEMONGGAEXYKNTQPIINDGS 393
OY 185 FELYSKLTVDSKRWQGNVSCSYMEALNNHYTKSLISPGK 228
DB 394 YFVYSKLVOKRSMWAGNFTCSVLHGLNHNHTEKILSHSPGK 437

RESULT 6
OY 095407 PRELIMINARY; PRT; 300 AA.
AC 095407;
RT 01-MAY-1999 (TEMBLrel. 10, Created)
RT 01-MAY-1999 (TEMBLrel. 10, Last sequence update)
RT 01-MAY-2000 (TEMBLrel. 13, Last annotation update)
DE DECOY RECEPTOR 3.
OS Homo sapiens (Human).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99087326.
RA Pitt R.M., Masters S.A., Lawrence D.A., Roy M., Kischkel F.C.,
RA Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T.,
RA Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L.,
RA Goddard A.D., Botstein D., Ashkenazi A.;
RT "Genomic amplification of a decoy receptor for Fas ligand in lung and
RT colon cancer.";
RL Nature 396:699-703(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE-BLOOD;
RX MEDLINE: 99253915.
RA Yu K.Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;
RT "A newly identified member of tumor necrosis factor receptor
RT superfamily (TR6) suppresses LIGHT-mediated apoptosis.";
RL J. Biol. Chem. 274:13733-13736(1999).
DR EMBL: AF104419; AAD03056.1; -.
DR EMBL: AF134240; AAD29688.1; -.
DR HSSP: P25942; ICDF.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001368; -.
DR PFAM: PF000020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
DR PROSITE: PS0186; EGF_2; UNKNOWN_1.
DR PROSITE: PS50050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 300 AA; 32679 MW; F90AE33718449AF CRC64;

Query Match
Best Local Similarity 19.3%; Score 433; DB 4; Length 300;
Matches 69; Conservative 29; Mismatches 63; Indels 0; Gaps 0;

OY 233 KYLYHDETSKOLDCNCPGTYLKOHCTAKMKTYCAPCPDHYTDSMHTSDECYCS 292
DB 34 PTYPMRDAETGERLVCAQCPCPGTFVORPCRDSPPTCGPCPPHYTQFNMYLERCYCNV 93
OY 293 VCKELOYVQECNRTNHRVCECKEGRYLEIEFCLKHSRCPGFGVVOAGTPEPRNTVCKR 352
DB 94 LCBREAEARACHATNHRACRRTGFFAHAGFLEHASCPCGAGVIAPIPSQNTQCOPC 153
OY 353 PDGFFSNETSCKAPCRKHTNCSVFGILLTQKGNATHDNCIS 393
DB 154 PGTFSSASSSSDQCPHRCNTAGLALNVPSSSHDTLCT 194

RESULT 7
OY 09PUS0 PRELIMINARY; PRT; 302 AA.
AC 09PUS0;
RT 01-MAY-2000 (TEMBLrel. 13, Created)
RT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
RT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
DE DECOY RECEPTOR.
OS Salvelinus fontinalis (Brook trout).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
OC Plectropterygii; Salmoniformes; Salmonidae; Salvelinus.
RN [1]
RP SEQUENCE FROM N.A.
RA Bode J., Goetz F.W.;
RT "A tumor necrosis factor receptor homolog is up-regulated in the brook
RT trout (Salvelinus fontinalis) cvary at the completion of ovulation.";
RL Biol. Reprod. 0:0-0(1999).
DR EMBL: AF156738; AAD56428.1; -.
DR INTERPRO: IPR000561; -.
DR INTERPRO: IPR001368; -.
DR PFAM: PF00020; TNFR_C6; 4.
DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.

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"A new antigen receptor gene family that undergoes rearrangement and RT extensive somatic diversification in sharks."

RT Nature 374:168-173(1995).
 RL EMBL: U18701; AAB48195.1; -
 DR INTERPRO: IPR003006; -
 DR INTERPRO: IPR003006; -
 DR PFM: PFM0047; 19; 6.
 DR PROSITE: PS00290; IG_MHC; UNKNOWN_3.
 KW Signal.
 FT SIGNAL 18
 FT CHAIN 19 684 NOVEL ANTIGEN RECEPTOR.
 SO SEQUENCE 684 AA; 75224 MW; 2FF9D2071CDA6DFD CRC64;

Query Match 12.1%; Score 272.5; DB 13; Length 684;
 Best Local Similarity 33.3%; Pred. No. 1.3e-15;
 Matches 71; Conservative 35; Mismatches 98; Indels 9; Gaps 7;

QY 20 SVFLPPKPKDLMISRPVETGVVDVSHEDPE-VKFNWVVDGVEVHNAKTRREGYN 78
 459 SVSLKRP-PFEIWTQQTATVCEIV--YSDLENIKVFWOVNGVERKKGVETONPEWSG 514

QY 79 STYRVSVLVTVHODWLVNGEKYCKVSNKALPAPIEKTISKAK-GQPREPOVYTLPPSRD 137
 515 SKSTIVSKLKMASEMDSCTEYVCLVEDSELPTVKASIRKANSQMHPRVYLHPSTD 574

QY 138 EL-TKNQVSLTCLVKGYPSPDIAYEWESNGO-PENNYKTPPVLDSDGSEFLYKSLTVDK 195
 575 EIDENSATLMLCLATNFHPAIIYGVGMANDTLDSGRYTVQDSEKSGSSFTVRLRLTA 634

QY 196 SRMQGVNVSVMHEALHNHYTOKSLSPCK 228
 DB 635 AEMNSDTTYSCLVGHPSL-NRDLIRSTKSNKG 666

RESULT 14
 QY606 PRELIMINARY; PRT; 616 AA.

AC QY606;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 DE INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF11A OR RANK.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE: 98032977.
 RA Anderson D.W., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Gilbert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- TISSUE SPECIFICITY: UBICUITOUS EXPRESSION WITH HIGH LEVELS IN
 CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
 CC GLAND.
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AF018253; AAB86809.1; -
 DR MIM: 603499; -
 DR INTERPRO: IPR001368; -
 DR PFM: PFM0020; TNFR_C6; 4.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS00652; TNFR_NGFR_2; 1.
 KW Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
 FT SIGNAL 1 22
 FT CHAIN 23 616
 FT DOMAIN 24 212
 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 213 233
 FT DOMAIN 234 616
 FT SIGNAL 235 616
 FT REPEAT 33 195
 FT REPEAT 33 69
 FT REPEAT 70 112
 FT REPEAT 113 152
 FT REPEAT 153 195
 FT DISULFID 34 46
 FT DISULFID 47 60
 FT DISULFID 50 68
 FT DISULFID 71 86
 FT DISULFID 92 112
 FT DISULFID 114 124
 FT DISULFID 126 133
 FT DISULFID 127 131
 FT DISULFID 154 169
 FT DISULFID 175 194
 FT CARBOHYD 105 105
 FT CARBOHYD 174 174
 SO SEQUENCE 616 AA; 66033 MW; E3DE9A7A08196F81 CRC64;

Query Match 11.2%; Score 252.5; DB 4; Length 616;
 Best Local Similarity 36.6%; Pred. No. 6.3e-14;
 Matches 56; Conservative 17; Mismatches 73; Indels 7; Gaps 4;

QY 248 CDKCPRTYKQKQCTAKTKVACPCPDHYTDSMHSDECLYCSVC--KELOYKQEC 304
 47 CNKEPKYMSKCTTSDSCVLCPCGDEYLDISNEEDKCL-LHKVDDTKALVAAYAG- 104

QY 305 NRTINRCECKEGRY--LEIEFLKHKSCPPGFGVQAGPRTYVKKRPPDGFSEETS 362
 105 NSTPRACCTAGYHMSQDCECCRNTECAPGLAQHPLQNDYCKPCLAGYFSDAFS 164

QY 363 SKAPCRKTKNSVGLLTQGNATHDNICGN 395
 DB 165 STDKCRWNTCTFLGKRVHEHGTSEKSDAVCSS 197

RESULT 15
 QY305 PRELIMINARY; PRT; 625 AA.

AC QY305;
 DT 01-JAN-1998 (Tremblrel. 05, Created)
 DT 01-JAN-1998 (Tremblrel. 05, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE RECEPTOR ACTIVATOR OF NF-KAPPA-B PRECURSOR (TNF-RELATED ACTIVATION-
 DE INDUCED CYTOKINE RECEPTOR) (RANK).
 GN TNFRSF11A OR RANK.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 [1]
 SEQUENCE FROM N.A.
 RX MEDLINE: 98032977.
 RA Anderson D.W., Maraskovsky E., Billingsley W.L., Dougall W.C.,
 RA Tometsko M.E., Roux E.R., Teepe M.C., Dubose R.F., Cosman D.,
 RA Gilbert L.;
 RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
 RT and dendritic-cell function.";
 RL Nature 390:175-179(1997).
 CC -1- FUNCTION: RECEPTOR FOR A CYTOKINE LIGAND KNOWN AS RANKL.
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (POTENTIAL).
 CC -1- SIMILARITY: CONTAINS A LA-NGFR/TNFR-TYPE CYSTEINE-RICH REGION.
 DR EMBL: AF019046; AAB86810.1; -
 DR HSP: P25942; 1CDF.
 DR MGD: MGT1314891; Tnfstfla.
 DR INTERPRO: IPR000561; -
 DR PFM: PFM0020; TNFR_C6; 3.
 DR PROSITE: PS00652; TNFR_NGFR_1; UNKNOWN_1.
 DR PROSITE: PS01186; EGF_2; UNKNOWN_1.

DR PROSITE: PS50050: TNFR_NGFR_2: 1.
KM Receptor; Glycoprotein; Transmembrane; Signal; Repeat.
FT SIGNAL 1
FT CHAIN 31 625
FT DOMAIN 31 214
FT TRANSMEM 215 235
FT DOMAIN 236 625
FT DOMAIN 34 196
FT REPEAT 34 70
FT REPEAT 71 114
FT REPEAT 115 153
FT REPEAT 154 196
FT DISULFID 35 47
FT DISULFID 48 61
FT DISULFID 51 69
FT DISULFID 72 87
FT DISULFID 93 113
FT DISULFID 115 125
FT DISULFID 127 134
FT DISULFID 128 152
FT DISULFID 155 170
FT DISULFID 176 195
FT CARBOHYD 106 106
FT CARBOHYD 175 175
SQ SEQUENCE 625 AA; 66621 MW; F8C1872E99511D8E CRC64;
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).

Query Match 11.2%; Score 252.5; DB 11; Length 625;
Best Local Similarity 36.6%; Pred. No. 6.4e-14;
Matches 56; Conservative 18; Mismatches 72; Indels 7; Gaps 4;

OY 248 CDKCPGTYLKGHCIAKMTVCAPCPDHYTDSWHTSDECLYCSPVC--KEIQYVKQEC 304
DB 48 CSRCEPGKTLSSKCTPTSDSVCLPCGPEYLDPTWNEDEKCL-LHKVCDAGKALVAV-DPG 105
OY 305 NRTNHNVCCEKEGRY--LEIEFCLKHRSCPPGFGVVOAGTPERNTVCKRCRCPDGFSENETS 362
DB 106 NHTADRRRCACGTAGHYMNSDCCECCRRNTEBCAPFGAQHPQLQNKDPTVCTPCLLGFFSDVFS 165
OY 363 SKAPCRKHTNCSVFGILLTQKGNATHDNICSGN 395
DB 166 STDCKCPMTNCTILGKLEAHOGTSESDVYCSSS 198

Search completed: December 27, 2000, 10:52:42
Job time: 73 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 27, 2000, 10:55:07 ; Search time 24.16 Seconds

(without alignments)
530.262 Million cell updates/sec

Title: US-09-389-545-8

Perfect score: 2246
Sequence: 1 MDKHTCPCPEAPPELLGSPS.....QKGNATHDNICSGNSESTOK 401

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 87993 seqs, 31947931 residues

Minimum number of hits satisfying chosen parameters: 87993

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 08

Maximum Match 1008
Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1233	54.9	330	1	GCL_HUMAN
2	1142.5	50.9	326	1	GCL_HUMAN
3	1135	50.5	327	1	GCL_HUMAN
4	1126	50.1	280	1	GCL_HUMAN
5	918.5	40.9	323	1	GC_RABIT
6	889	39.6	329	1	GC2_CAVO
7	845.5	37.6	329	1	GC2_MOUSE
8	838	37.3	333	1	GC3_MOUSE
9	835.5	37.2	333	1	GC3_MOUSE
10	818.5	36.4	326	1	GCL_RAT
11	817.5	36.4	324	1	GCL_MOUSE
12	812.5	36.2	333	1	GCL_MOUSE
13	809.5	36.0	329	1	GC2_MOUSE
14	809	36.0	330	1	GCA_MOUSE
15	804	35.8	339	1	GCA_MOUSE
16	802	35.7	335	1	GCA_MOUSE
17	785.5	35.0	322	1	GCA_RAT
18	779	34.7	336	1	GCB_MOUSE
19	774	34.5	405	1	GCB_MOUSE
20	774	34.5	405	1	GCB_MOUSE
21	774	34.5	405	1	GCB_MOUSE
22	774	34.5	405	1	GCB_MOUSE
23	774	34.5	405	1	GCB_MOUSE
24	774	34.5	405	1	GCB_MOUSE
25	774	34.5	405	1	GCB_MOUSE
26	774	34.5	405	1	GCB_MOUSE
27	774	34.5	405	1	GCB_MOUSE
28	774	34.5	405	1	GCB_MOUSE
29	774	34.5	405	1	GCB_MOUSE
30	774	34.5	405	1	GCB_MOUSE
31	774	34.5	405	1	GCB_MOUSE
32	774	34.5	405	1	GCB_MOUSE
33	774	34.5	405	1	GCB_MOUSE

ALIGNMENTS

34	303	13.5	438	1	HVC2_HETFR	P23085 heterodontu
35	299.5	13.3	299	1	ALC_RABIT	P201879 oryctolagus
36	293.5	13.1	438	1	HVC3_HETFR	P23087 heterodontu
37	287.5	12.8	446	1	MOE_CHICK	P201875 gallus galli
38	284	12.6	289	1	CD40_MOUSE	P227512 mus musculus
39	282.5	12.6	393	1	HVC3_HETFR	P23086 heterodontu
40	278.5	12.4	461	1	HVC4_HETFR	P23088 heterodontu
41	278	12.4	370	1	HVC1_HETFR	P23084 heterodontu
42	276	12.3	353	1	ALC1_HUMAN	P201876 homo sapien
43	271.5	12.1	353	1	ALC1_GORGO	P207518 gorilla gor
44	271	12.1	340	1	ALC2_HUMAN	P01877 homo sapien
45	264	11.8	277	1	CD40_HUMAN	P25942 homo sapien

ALIGNMENTS

RESULT 1

GCL_HUMAN

STANDARD;

PRT;

330 AA.

AC

P01877;

21-JUL-1986 (Rel. 01, Created)

21-JUL-1986 (Rel. 01, Last sequence update)

15-JUL-1999 (Rel. 38, Last annotation update)

IG GAMA-1 CHAIN C REGION.

IGHG1.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.

RN

RP

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RA Edelman G.M.;

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GCL_HUMAN
 ID GCL_HUMAN
 AC P01857
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE IG GAMMA-1 CHAIN C REGION.
 GN IGHG1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE: 82274238.
 RA Ellison J.W., Berson B.J., Hood L.E.;
 RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";
 RL Nucleic Acids Res. 10:4071-4079(1982).
 RN [2]
 RP SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).
 RX MEDLINE: 71064024.
 RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,
 RA Wexel M.J., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino
 acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";
 RL Biochemistry 9:3161-3170(1970).
 RN [3]
 RP SEQUENCE OF 136-329 (EU).
 RX MEDLINE: 71064025.
 RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,
 RA Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino
 acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";
 RL Biochemistry 9:3171-3181(1975).
 RN [4]
 RP SEQUENCE (MYELOMA PROTEIN N.E).
 RX MEDLINE: 77070269.
 RA Ponting H., Hilschmann N.;
 RT "The rule of antibody structure. The primary structure of a
 monoclonal IgG1 immunoglobulin (myeloma protein Nle). III. The
 chymotryptic peptides of the H-chain, alignment of the tryptic
 peptides and discussion of the complete structure.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).
 RN [5]
 RP SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.
 RX MEDLINE: 83289131.
 RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;
 RT "Three-dimensional structure determination of antibodies. Primary
 structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";
 RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).
 RN [6]
 RP DISULFIDE BONDS.
 RX MEDLINE: 71064027.
 RA Gall W.E., Edelman G.M.;
 RT "The covalent structure of a human gamma G-immunoglobulin. X.
 intrachain disulfide bonds."

Biochemistry 9:3188-3196(1970).

RL [7] DISULFIDE BONDS.

RP MEDLINE: 77070267.

RA Dieker L., Schwarz J., Relchel W., Hilschmann N.;

RT "Rule of antibody structure. The primary structure of a monoclonal

RT IgG1 immunoglobulin (myeloma protein Nle), I: Purification and

RT characterization of the protein, the L- and H-chains, the

RT cyanogen bromide cleavage products, and the disulfide bridges.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).

RN [8]

RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).

RX MEDLINE: 81208100.

RA Delsenhofer J.;

RT "Crystallographic refinement and atomic models of a human Fc fragment

RT and its complex with fragment B of protein A from *Staphylococcus*

RT aureus at 2.9- and 2.8-A resolution.";

RL Biochemistry 20:2361-2370(1981).

CC -I- MISCELLANEOUS: NIE HAS THE GIM(17) ALLOTYPIC MARKER, 97-K, & THE

CC GIM(1) MARKERS, 239-D & 241-L. KOL & EU SEQUENCES HAVE THE GIM(3)

CC MARKER & THE GIM (NON-1) MARKERS.

CC -I- MISCELLANEOUS: NIE ALSO DIFFERS IN THE AMIDATION STATES OF

CC 35,116,198,269 & 272.

CC -I- MISCELLANEOUS: EU ALSO DIFFERS IN THE AMIDATION STATES OF RESIDUES

CC 155, 166, 177, 195, 198, 269, AND 272 AND IN THE ORDER OF RESIDUES

CC 268-272.

CC -I- MISCELLANEOUS: KOL ALSO DIFFERS IN THE AMIDATION STATES OF

CC RESIDUES 198,267&272.

CC -----

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CC or send an email to license@isb-sib.ch).

CC -----

CC EMBL: J00228; AAC82527.1; ALT_INIT.

DR PIR: A02146; GHHT.

DR PDB: 1FC1; 15-JUL-92.

DR PDB: 1FC2; 15-JUL-92.

DR MIM: 147100; -

DR INTERPRO: IPR000495; -

DR INTERPRO: IPR003006; -

DR PFAM: PF00047; 1g; 3.

DR PROSITE: PS00290; 1G_MHC; 2.

DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;

DR 3D-structure.

NON_TER 1 1

DOMAIN 99 98 CH1.

DOMAIN 111 110 HINGE.

DOMAIN 224 223 CH2.

DOMAIN 224 330 CH3.

DISULFID 27 83

DISULFID 103 103 INTERCHAIN (WITH LIGHT CHAIN).

DISULFID 109 109 INTERCHAIN (WITH HEAVY CHAIN).

DISULFID 112 112 INTERCHAIN (WITH HEAVY CHAIN).

DISULFID 144 204

DISULFID 250 308

CARBOHYD 180 180

VARIANT 97 97

VARIANT 239 239

VARIANT 241 241

VARIANT 241 241

MOD_RES 330 330

STRAND 123 126

HELIX 130 134

TURN 136 137

STRAND 141 148

STRAND 158 162

TURN 163 164

REMOVED POST-TRANSLATIONALLY.

FT STRAND 165 166

FT STRAND 175 178

FT STRAND 183 190

FT HELIX 193 197

FT TURN 198 199

FT STRAND 202 206

FT STRAND 215 219

FT STRAND 227 227

FT STRAND 230 234

FT HELIX 238 240

FT TURN 241 242

FT STRAND 245 256

FT STRAND 260 266

FT TURN 267 268

FT STRAND 274 276

FT STRAND 280 281

FT TURN 283 284

FT STRAND 287 296

FT HELIX 297 301

FT TURN 302 303

FT STRAND 306 312

FT TURN 313 314

FT TURN 316 317

FT STRAND 320 324

SEQUENCE 330 AA; 36106 MM; 3770E106C2FA3D CRC64;

Query Match 54.9%; Score 1233; DB 1; Length 330;

Best Local Similarity 100.0%; Pred. No. 8; 9e-79;

Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKTHCPCPAPELIGGSVFLFPKPKDTLMISRTPEVTCVYVDVSHEDPEVFNMTYVD 61

DB 104 DKTHCPCPAPELIGGSVFLFPKPKDTLMISRTPEVTCVYVDVSHEDPEVFNMTYVD 163

QY 62 GVEVNAKTKPREEQYNSTYRVSVYTLVHODMNGEKYCKVSKNALPAPERTISAK 121

DB 164 GVEVNAKTKPREEQYNSTYRVSVYTLVHODMNGEKYCKVSKNALPAPERTISAK 223

QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 181

DB 224 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLD 283

QY 182 DGSFPLSKITVDKSRMOQGVFSGSVVHEALHNHYTQKSLSLSPGK 228

DB 284 DGSFPLSKITVDKSRMOQGVFSGSVVHEALHNHYTQKSLSLSPGK 330

RESULT 2

GC2_HUMAN STANDARD: PRT; 326 AA.

ID GC2_HUMAN

AC P01859;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DE 15-JUL-1999 (Rel. 38, Last annotation update)

GN IG GAMA-2 CHAIN C REGION.

OS HOMO SAPIENS (HUMAN).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE: 82197621.

RA Ellison J.W., Hood L.E.;

RT "Linkage and sequence homology of two human immunoglobulin gamma

RT heavy chain constant region genes.";

RL Proc. Natl. Acad. Sci. U.S.A. 79:1984-1988(1982).

RN [2]

RP SEQUENCE OF 1-325 (MYELOMA PROTEIN TIL).

RX MEDLINE: 81007873.

RA Wang A.-C., Tung E., Fudenberg H.H.;

RT "The primary structure of a human IgG2 heavy chain: genetic,


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RT half-cystine joining heavy and light chains."
RL Biochemistry 10:18-25(1971).
RN [3]
RP SEQUENCE OF 69-133 AND 312-329.
RX MEDLINE; 71058486.
RA Turner K.J., Gebra J.J.;
RT "Structure of heavy chain from strain 13 guinea pig
immunoglobulin G(2). II. Amino acid sequence of the carboxyl-terminal
and hinge region cyanogen bromide fragments."
RL Biochemistry 10:9-17(1971).
RN [4]
RP SEQUENCE OF 134-226.
RX MEDLINE; 75036072.
RA Tracey D.E., Gebra J.J.;
RT "Primary structure of the CH2 homology region from guinea pig IgG2
antibodies."
RL Biochemistry 13:4796-4803(1974).
RN [5]
RP SEQUENCE OF 227-311.
RX MEDLINE; 75036073.
RA Trischmann T.M., Gebra J.J.;
RT "Primary structure of the CH3 homology region from guinea pig IgG2
antibodies."
RL Biochemistry 13:4804-4811(1974).
RN [6]
RP DISULFIDE BONDS.
RX MEDLINE; 71058474.
RA Oliveira B., Lamm M.E.;
RT "Interchain disulfide bridges of guinea pig gamma-2-immunoglobulin."
RL Biochemistry 10:26-31(1971).
CC -1- MISCELLANEOUS: THIS CHAIN WAS ISOLATED FROM POOLED SERUM OF STRAIN
CC 13 INBRED GUINEA PIGS.
DR PIR; A02151; G2GP.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein.
FT NON_TER 1
FT DISULFID 16 16 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 28 28
FT DISULFID 105 105 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .).
FT DISULFID 248 308
FT SEQUENCE 329 AA; 36074 MW; 5D231B7164D1FBA9 CRC64;

Query Match 39.6%; Score 889; DB 1; Length 329;
Best Local Similarity 72.3%; Pred. No. 6, 1e-55;
Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

OY 6 TCRPAPBELLGSPVFLFPPKPKDLMISRPEYTCVYVDVSHDEPEKFNMYDGYEV 65
DB 106 TCRPAPBELLGSPVFLFPPKPKDLMISRPEYTCVYVDVSHDEPEKFNMYDGYEV 165
OY 66 HNAKTKPREOYNSTYRVVSVLTVLHODWLNKREKCKVSNKALPAPIEKTISKAKGPR 125
DB 166 GNAETKPREOYNSTYRVVSVLTVLHODWLNKREKCKVSNKALPAPIEKTISKAKGPR 225
OY 126 EFQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGPR--ENNYKTPPVLDSDG 183
DB 226 MDDVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGPR--ENNYKTPPVLDSDG 285
OY 184 SFFLYSKLTVDKSRMOQGVNFCVYVHEALHNHYTOKSLSPG 227
DB 286 SFFLYSKLTVDKSRMOQGVNFCVYVHEALHNHYTOKSLSPG 329

RESULT 7
GC3_MOUSE

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ID GC3_MOUSE STANDARD; PRT; 329 AA.
AC P22436;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, SECRETED FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE; 85027161.
RA Wels J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
RA Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene."
RL EMBO J. 3:2041-2046(1984).
CC -----
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CC -----
CC EMBL; J00451; -; NOT_ANNOTATED_CDS.
DR PIR; B02156; G3MSC.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KW Immunoglobulin C region; glycoprotein; Transmembrane;
KW Alternative splicing.
FT NON_TER 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 113 HINGE.
FT DOMAIN 114 223 CH2.
FT DOMAIN 224 327 CH3.
FT SEQUENCE 329 AA; 36228 MW; F45827174182BAD6 CRC64;

Query Match 37.6%; Score 845.5; DB 1; Length 329;
Best Local Similarity 67.0%; Pred. No. 6, 3e-52;
Matches 150; Conservative 34; Mismatches 37; Indels 3; Gaps 1;

OY 8 PP---CPAPBELLGSPVFLFPPKPKDLMISRPEYTCVYVDVSHDEPEKFNMYDGYEV 64
DB 106 PGSSCPPEGNITLGGPSVFLFPPKPKDLMISRPEYTCVYVDVSHDEPEKFNMYDGYEV 165
OY 65 VHNKTKPREOYNSTYRVVSVLTVLHODWLNKREKCKVSNKALPAPIEKTISKAKGPR 124
DB 166 VHNKTKPREOYNSTYRVVSVLTVLHODWLNKREKCKVSNKALPAPIEKTISKAKGPR 225
OY 125 REPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOENNYKTPPVLDSDGS 184
DB 226 QTPQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEWESNGOENNYKTPPVLDSDGS 285
OY 185 SFFLYSKLTVDKSRMOQGVNFCVYVHEALHNHYTOKSLSPG 228
DB 286 YFLYSKLTVDKSRMOQGVNFCVYVHEALHNHYTOKSLSPG 329

RESULT 8
GCB_RAT
ID GCB_RAT STANDARD; PRT; 333 AA.
AC P20761;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2B CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0018; PS0018.
DR INTERPRO: IPR000495; -.
DR PIR: A02155; G3MSM.
DR INTERPRO: IPR003006; -.
DR PIR: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region.
FT DISULFID 1 15
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SO SEQUENCE 333 AA; 36497 MW; 55F8B64D48DA60A6 CRC64;

Query Match 37.3%; Score 838; DB 1; Length 333;
Best Local Similarity 66.4%; Pred. No. 2,1e-51;
Matches 148; Conservative 33; Mismatches 42; Indels 0; Gaps 0;

QY 6 TCCPCAPPELLGGSVFLPPKPKDILMISRTPEVTCVVDVSHDEPFVNMVYDGEV 65
DB 111 TCHKRPVELLGGPSVFIFPPKPKDILISQNAKTCVVDVSEEPDQVGFVANNVY 170
QY 66 HNAKTRPEEOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGQPR 125
DB 171 HPAQTOPREEOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGLVR 230
QY 126 EQOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPNKYKTPPVLDSDGSF 185
DB 231 KPOYVMPGPTEQLTEQVYSLTCLTSGFLPNDIGVMTSNGHIEKNYKTEPVMDSDGSF 290
QY 186 FLYSKLTVDKSRMOQGNVFCSVMEALHNHYTKSLSPGK 228
DB 291 FMYSKLTNVRSRMDSRAPVFCVHVEGLHNHVEKSISSPPK 333

RESULT 9
GC3M_MOUSE STANDARD: PRT: 398 AA.
ID GC3M_MOUSE P03987;
DT 23-OCT-1986 (Rel. 02, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-3 CHAIN C REGION, MEMBRANE-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 85027161.
RA Weis J.A., Word C.J., Rimm D., Der-Balan G.P., Martinez H.M.,
Tucker P.W., Blattner F.R.;
RT "Structural analysis of the murine IgG3 constant region gene.";
RL EMBO J. 3:2041-2046(1984).
RN [2]
RP SEQUENCE OF 328-398 FROM N.A.
RX MEDLINE: 84041483.
RA Komaromy M., Clayton L., Rogers J., Robertson S., Kettman J.,
Wall R.;
RT "The structure of the mouse immunoglobulin in gamma 3 membrane gene
segment.";
RL Nucleic Acids Res. 11:6775-6785(1983).
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CC -----
DR EMBL: J00451; AAB59655.1; -.
DR EMBL: V01526; CAA24767.1; ALT_SEQ.
DR PIR: A02155; G3MSM.
DR INTERPRO: IPR000495; -.
DR PIR: PF00047; 19; 3.
DR INTERPRO: IPR003006; -.
DR PIR: PS00290; IG_MHC; 1.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein;
FT DISULFID 1 15
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 80
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 115 115 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 147 207
FT DISULFID 253 311
SO SEQUENCE 398 AA; 43929 MW; CF7F264B50A41B95 CRC64;

Query Match 37.2%; Score 835.5; DB 1; Length 398;
Best Local Similarity 66.2%; Pred. No. 3,9e-51;
Matches 149; Conservative 34; Mismatches 39; Indels 3; Gaps 1;

QY 8 PP--CPAPPELLGGSVFLPPKPKDILMISRTPEVTCVVDVSHDEPFVNMVYDGEV 64
DB 106 PGSSCPGNILGGSVFLPPKPKDILMISLTPVTCVVDVSDDDVHSMFVDKKE 165
QY 65 VNAKTRPEEOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGQPR 124
DB 166 VHTAMTOPREAOYNSTYRVSVLVTLVHODWLNGEKYCKVSNKALPAPIERTISAKGRRA 225
QY 125 REPOYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPNKYKTPPVLDSDGS 184
DB 226 QTPQYVTLPPSRDELTKNOVSLTCLVKGFPSPDIAYEVESNGQPNKYKTPPVLDSDGS 285
QY 185 FLYSKLTVDKSRMOQGNVFCSVMEALHNHYTKSLSPGK 229
DB 286 YFLYSKLTVDKSRMOQGNVFCSVMEALHNHYTKSLSPGK 330

RESULT 10
GC1_RAT STANDARD: PRT: 326 AA.
ID GC1_RAT AC P20759;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 89232738.
RA Brueggemann M.;
RT "Evolution of the rat immunoglobulin gamma heavy-chain gene family.";
RL Gene 74:473-482(1988).
DR PIR: PS0017; PS0017.
DR INTERPRO: IPR000495; -.
DR PIR: PF00047; 19; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; glycoprotein.

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FT NON_TER 1 1
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 112 HINGE.
FT DOMAIN 113 113 CH2.
FT DOMAIN 219 326 CH3.
FT DISULFID 27 82 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 102 102 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 106 106 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 140 200
FT DISULFID 246 304
FT CARBOHYD 176 176
SQ SEQUENCE 326 AA; 35946 MW; 013BAB5EF49B5DA CRC64;

Query Match
Best Local Similarity 36.4%; Score 818.5; DB 1; Length 326;
Matches 142; Conservative 41; Mismatches 35; Indels 7; Gaps 2;

7 CPGCPABELLG---PSVFLPPKPKDITLMISRTPEVTCVYVDSHEDPEVKNWYDGY 63
106 CKPC---ICTGEVSSVFIFPPKPKDVLITLTPKVTQVVDISODDPEHFSWFVDV 161
64 EVHNAKTPREEDQNSTYRYVSVLTGLHODWLNKGEKCKVSKALPAPLEKTIKRAKQ 123
162 EVHNAKTPREEDQNSTYRYVSVLTGLHODWLNKGEKCKVSKALPAPLEKTIKRAKQ 221
124 PREPOVYTLPPSDELTKNVSLTCLVKGFPSPDAVEMESNGOPENNYKTPPVLDSDG 183
222 TVPHTVYTPMPTKEEMTQNEVSTICWKGFPDVIYEMQNGOPQENYKTPPTMDTDG 281
184 SFLLYSKLTVDKSRMOQGNFSCSVNHEALHNHYTKSLSLSGK 228
282 SYFLSKLTNVKKEKMOQGNFTCSVLHGLHNHTEKSLSHSPGK 326

RESULT 11
GCL_MOUSE STANDARD; PRT; 324 AA.
AC P01868;
DC 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-1 CHAIN C REGION.
OS Mus musculus (Mouse).
NC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
[1]
NP SEQUENCE FROM N.A.
RX MEDLINE: 80045036.
RA Honjo T., Obata M., Yamawaki-Kataoka Y., Kataoka T., Kawakami T.,
Takahashi N., Mano Y.;
RT "Cloning and complete nucleotide sequence of mouse immunoglobulin
gamma 1 chain gene."
RT Cell 18:559-568(1979).
RN [2]
RP SEQUENCE OF 76-324 FROM N.A. (MYELOMA PROTEIN MOPC 31C).
RX MEDLINE: 80202559.
RA Obata M., Yamawaki-Kataoka Y., Takahashi N., Kataoka T., Shimizu A.,
Mano Y., Seidman J.G., Peterlin B.M., Leder P., Honjo T.;
RT "Immunoglobulin gamma 1 heavy chain gene: structural gene sequences
cloned in a bacterial plasmid."
RT Gene 9:87-97(1980).
RN [3]
RP SEQUENCE OF 70-322 FROM N.A. (MYELOMA PROTEIN MOPC 21).
RX MEDLINE: 80012837.
RA Rogers J., Clarke P., Salsner W.;
RT "Sequence analysis of cloned cDNA encoding part of an immunoglobulin
heavy chain."
RT Nucleic Acids Res. 6:3305-3321(1979).
RN [4]
RP SEQUENCE (MYELOMA PROTEIN MOPC 21).

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RX MEDLINE: 78242288.
RA Adetungbo K.;
RT "Evolution of immunoglobulin subclasses. Primary structure of a
murine myeloma gamma1 chain."
RT J. Biol. Chem. 253:6068-6075(1978).
RN [5]
RP DISULFIDE BONDS (MOPC 21).
RX MEDLINE: 73008889.
RA Svastl J., Milstein C.;
RT "The disulphide bridges of a mouse immunoglobulin G1 protein."
RT Biochem. J. 126:837-850(1972).
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CC -----
DR EMBL: V00793; CA24172.1; -
DR EMBL: V00793; CA24173.1; -
DR EMBL: V00793; CA24174.1; -
DR EMBL: V00793; CA24175.1; -
DR EMBL: V00793; CA24176.1; -
DR PIR: A02159; GIMS.
DR MGD: MGI:96446; IGH-4.
DR INTERPRO: IPR000495; -
DR INTERPRO: IPR003006; -
DR PFAM: PF00047; Ig; 3.
DR PROSITE: PS00290; IG_MHC; 1.
KW Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
KW Alternative splicing.
FT NON_TER 1 97
FT DOMAIN 1 97 CH1.
FT DOMAIN 98 110 HINGE.
FT DOMAIN 111 217 CH2.
FT DOMAIN 218 324 CH3.
FT DISULFID 27 82
FT DISULFID 102 102 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 104 104 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 109 109 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 138 198 INTERCHAIN (WITH A HEAVY CHAIN).
FT CARBOHYD 174 174
FT DISULFID 244 302
FT MOD_RES 324 324 REMOVED POST-TRANSLATIONALLY.
FT CONFLICT 276 276 N -> D (IN REF. 3).
FT CONFLICT 278 278 N -> D (IN REF. 3).
SQ SEQUENCE 324 AA; 35704 MW; A338812F3D1F2C93 CRC64;

Query Match
Best Local Similarity 36.4%; Score 817.5; DB 1; Length 324;
Matches 140; Conservative 44; Mismatches 35; Indels 5; Gaps 2;

7 CPGCPABELLG---PSVFLPPKPKDITLMISRTPEVTCVYVDSHEDPEVKNWYDGY 64
104 CKPCICTPEV---SSVFLPPKPKDVLITLTPKVTQVVDISODDPEHFSWFVDV 160
65 VHNNAKTPREEDQNSTYRYVSVLTGLHODWLNKGEKCKVSKALPAPLEKTIKRAKQ 124
161 VHTAQTQPREEDQNSTYRYVSVLTGLHODWLNKGEKCKVSKALPAPLEKTIKRAKQ 220
125 REPQVYTLPPSDELTKNVSLTCLVKGFPSPDAVEMESNGOPENNYKTPPVLDSDG 184
221 KAPOVYTLPPSDELTKNVSLTCLVKGFPSPDAVEMESNGOPENNYKTPPVLDSDG 280
185 SFLLYSKLTVDKSRMOQGNFSCSVNHEALHNHYTKSLSLSGK 228
281 YFYSKLTNVKKEKMOQGNFTCSVLHGLHNHTEKSLSHSPGK 324

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FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 111 111 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 113 113 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 143 203
FT DISULFID 249 307
SQ SEQUENCE 329 AA; 36571 MW; 5FCD7B7933850773 CRC64;

Query Match 36.0%; Score 809.5; DB 1; Length 329;
Best Local Similarity 63.8%; Pred. No. 2e-49;
Matches 143; Conservative 41; Mismatches 37; Indels 3; Gaps 1;

OY 8 CPPELLGSPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNMYDVGVE 64
DB PPTDCSDNDNGRPVSFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNMYDVGVE 165
OY 65 VHNATKPREDOYNSTRVSVTLVHODMLNGKEYCKVSNKALPAPIETISKAKGP 124
166 VTAQTQPHEDQNGTFRVSVTLHIOHODMWSGKEFKCKVNNKDLPSPIEKTISKPRGA 225
OY 125 REPQYITLPPSRDELTKNOVSLTCLVKGFPDIAVWESNGQPNNTKTPPYLDSGS 184
DB 226 RPPQYITLPPSRDESKKNVSLTCLVKGFPDIAVWESNGQPNNTKTPPYLDSGS 285
OY 185 FFLYSKLTVDKSRMOQGVFSCVYHHEALHNHYTKSLSPGK 228
DB 286 YFLYSKLTVDKSRMOQGVFSCVYHHEALHNHYTKSLSPGK 329

RESULT 14
ID GCAM_MOUSE STANDARD; PRT; 330 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, A ALLELE.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 81076554.
RA Sikorav J.-L., Aufray C., Rougeon F.;
RT "Structure of the constant and 3' untranslated regions of the murine
RT Balb/c gamma 2a heavy chain messenger RNA."
RL Nucleic Acids Res. 8:3143-3155(1980).
RN (2)
RP SEQUENCE FROM N.A.
RX MEDLINE; 81198976.
RA Yamawaki-Kataoka Y., Miyata T., Honjo T.;
RT "The complete nucleotide sequence of mouse immunoglobulin gamma 2a gene
RT and evolution of heavy chain genes: further evidence for intervening
RT sequence-mediated domain transfer."
RL Nucleic Acids Res. 9:1365-1381(1981).
RN (3)
RP SEQUENCE FROM N.A.
RX MEDLINE; 81223894.
RA Olio R., Aufray C., Morchamps C., Rougeon F.;
RT "Comparison of mouse immunoglobulin gamma 2a and gamma 2b chain genes
RT suggests that exons can be exchanged between genes in a multigenic
RT family."
RL Proc. Natl. Acad. Sci. U.S.A. 78:2442-2446(1981).
RN (4)
RP MYELOMA PROTEIN MOPC 173.
RX Bourgois A., Fougereau M., Rocca-Serra J.;
RT "Determination of the primary structure of a mouse IgG2a
RT immunoglobulin: amino-acid sequence of the Fc fragment. Implications
RT for the evolution of immunoglobulin structure and function."
RL Eur. J. Biochem. 43:423-435(1974).
RN (5)

```

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RP DISULFIDE BONDS.
RX MEDLINE; 73056887.
RA de Preval C., Fougereau M.;
RT "Determination of the primary structure of a mouse gamma G2a
RT immunoglobulin. Identification of the disulfide bridges."
RL Eur. J. Biochem. 30:452-462(1972).
CC -----
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CC -----
DR EMBL; V00798; CAA24178.1; -.
DR PIR; A02152; GZMSA.
DR INTERPRO; IPR000495; -.
DR INTERPRO; IPR003006; -.
DR PFAM; PF00047; 1g; 3.
DR PROSITE; PS00290; IG_MHC; 1.
KM Immunoglobulin domain; Immunoglobulin C region.
FT NON_TER 1 1
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT MOD_RES 330 330
SQ SEQUENCE 330 AA; 36389 MW; B84361C5445A6864 CRC64;

Query Match 36.0%; Score 809; DB 1; Length 330;
Best Local Similarity 65.2%; Pred. No. 2.2e-49;
Matches 146; Conservative 30; Mismatches 46; Indels 2; Gaps 1;

OY 7 CPPELLGSPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNMYDVGVE 64
DB 107 CPPELLGSPVFLFPKPKDMLISRTPEVTCVVDVSHEDPEVKFNMYDVGVE 166
OY 65 VHNATKPREDOYNSTRVSVTLVHODMLNGKEYCKVSNKALPAPIETISKAKGP 124
DB 167 VHTAQTHREDVNSTLRVSVTLHIOHODMWSGKEFKCKVNNKDLPSPIEKTISKPRGSV 226
OY 125 REPQYITLPPSRDELTKNOVSLTCLVKGFPDIAVWESNGQPNNTKTPPYLDSGS 184
DB 227 RPPQYITLPPSRDESKKNVSLTCLVKGFPDIAVWESNGQPNNTKTPPYLDSGS 286
OY 185 FFLYSKLTVDKSRMOQGVFSCVYHHEALHNHYTKSLSPGK 228
DB 287 YFLYSKLTVDKSRMOQGVFSCVYHHEALHNHYTKSLSPGK 330

RESULT 15
ID GCAM_MOUSE STANDARD; PRT; 399 AA.
AC P01863;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE IG GAMMA-2A CHAIN C REGION, MEMBER-BOUND FORM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE; 82222190.
RA Yamawaki-Kataoka Y., Nakai S., Miyata T., Honjo T.;
RT "Nucleotide sequences of gene segments encoding membrane domains of
RT immunoglobulin gamma chains."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2623-2627(1982).

```

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CC -1- ALTERNATIVE PRODUCTS: CELL LINES PRODUCING IGG CONTAIN TWO MRNA
CC SPECIES FOR IG GAMMA CHAINS. THE MAJOR SPECIES ENCODES SECRETED
CC GAMMA CHAINS. A LESS ABUNDANT SPECIES APPEARS TO ENCODE MEMBRANE-
CC BOUND CHAINS IN THAT IT CONTAINS AN ALTERNATIVE 3' END, ENCODED
CC IN SEPARATE EXONS, THAT IS HOMOLOGOUS WITH THE MEMBRANE-BOUND
CC SEGMENT OF MU CHAINS.
CC -1- MISCELLANEOUS: THE SEQUENCE OF RESIDUES 1-329 IS ASSUMED TO BE
CC IDENTICAL WITH THE CORRESPONDING REGION OF THE SECRETED FORM OF
CC THE A ALLELE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL: J00471; AAB59661.1; ALT_INIT.
DR PIR: A02154; G2MSAM.
DR MGD: MG1:96443; IGH-1.
DR INTERPRO: IPR000495; -.
DR INTERPRO: IPR003006; -.
DR PRAM: PF00047; 19; 3.
DR PROSITE: PS00290; IGH_MHC; 1.
DR Immunoglobulin domain; Immunoglobulin C region; Glycoprotein;
DR Transmembrane; Alternative splicing.
KW NON_TER 1 1.
FT DISULFID 15 15 INTERCHAIN (WITH A LIGHT CHAIN).
FT DISULFID 27 82
FT DISULFID 107 107 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 110 110 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 112 112 INTERCHAIN (WITH A HEAVY CHAIN).
FT DISULFID 144 204
FT DISULFID 250 308
FT TRANSMEM 346 363
FT DOMAIN 364 399
FT CARBOHYD 180 180
FT SEQUENCE 399 AA: 44020 MW: 4C38138BFAD3FF0 CRC64;
SQ
Query Match 35.88; Score 804; DB 1; Length 399;
Best Local Similarity 65.08; Pred. No. 5.9e-49;
Matches 145; Conservative 30; Mismatches 46; Indels 2; Gaps 1;
QY - 7 CYP--CPAPELLGGPSVFLPPPKRDTLMISRTPEVTCVVDVSHEDPEVFNMYVDGVE 64
107 CPGCKCPAPNLGGPSVFIFPPKIKDVLIMISLPIVTCVVDVSEDDPDVQISMFVNV 166
65 VHNAKTRPREDQVNSTYRVVSVLTVLHODVLNGEKYCKVSNKALPAPIERTISKAKGP 124
167 VHTAQOTIHREDYNSLTRVVSALPIOHODWMSGKFKCKVNNKDLPAPIERTISKPGSV 226
QY 125 REPQVYVLPSPRDELTKNOVSLTCLVGEFSDIAYEMESNGOPENNYKTPPLDSDGS 184
DB 227 RAPQVYVLPPEEEMTKQVTLTCMTVDPEPEDIYVEPTNNGKTELNKTEPVLSDGS 286
QY 185 FFYYSKLTVDKSRWQGNVFCSVYHREALHNHYTKSLSPG-227
DB 287 YFMYSKLTVEKKMVERNSYSCSVYHGLNHNHTTKSFRTPG 329
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Search completed: December 27, 2000, 10:55:08
Job time: 210 sec

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A:Molecule type: DNA
A:Residues: 1-330 <ELL>
A:Cross-references: EMBL:Z17370
A:Note: this sequence has the Gln(17) allotypic marker, 97-Lys, and the Gln(1) markers,
A:Note: Lys-330 is removed after translation
R:Harris, L.J.
Submitted to the EMBL Data Library, October 1992
A:Reference number: S33904
A:Accession: S36861
A:Molecule type: DNA
A:Residues: 2-330 <HAR>
A:Cross-references: EMBL:Z17370
R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.
Cell 29, 671-679, 1982
A:Title: Structure of human immunoglobulin gamma genes: implications for evolution of a
A:Reference number: S33887; MUID:83001943
A:Accession: S33887
A:Molecule type: DNA
A:Residues: 88-113:235-330 <TAK>
A:Cross-references: EMBL:Z17370
R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Maxdall, M.J.; Edelman,
Biochemistry 9, 3161-3170, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VII. Amino acid sequen
A:Reference number: A90563; MUID:71064024
A:Contents: myeloma protein Eu
A:Accession: B90563
A:Molecule type: Protein
A:Residues: 1-96, 'R', 98-135 <CON>
A:Note: this sequence has the Gln(3) marker, 97-Arg
R:Rutishauser, U.; Cunningham, B.A.; Bennett, G.; Konigsberg, W.H.; Edelman, G.M.
Biochemistry 9, 3171-3181, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. VIII. Amino acid sequen
A:Reference number: A90564; MUID:71064025
A:Contents: Eu
A:Accession: A90564
A:Molecule type: Protein
A:Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240,
A:Note: this sequence has the Gln(non-1) markers, 239-Glu and 241-Met
R:Ponstingl, H.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976
A:Title: Die Primerstruktur elnes monoklonalen IgG1-Immunglobulins (Myelomprotein Nle),
Igen Primerstruktur.
A:Reference number: A91668; MUID:77070269
A:Contents: myeloma protein Nle
A:Accession: B91668
A:Molecule type: Protein
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'Q', 117-197, 'D', 199-238, 'D', 240, 'V', 242-268, 'E', 27
A:Note: this sequence has the Gln(17) and Gln(1) markers
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983
A:Title: Die Primerstruktur des kristallisierbaren monoklonalen Immunglobulins IgG1 KOI
A:Reference number: A91723; MUID:83289131
A:Contents: myeloma protein KOI; disulfide bonds
A:Accession: A91723
A:Molecule type: Protein
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'W', 242-266, 'D', 268-271, 'D', 273-330 <SCH
A:Note: this sequence has the Gln(3) and Gln(non-1) markers
R:Gall, W.E.; Edelman, G.M.
Biochemistry 9, 3188-3196, 1970
A:Title: The covalent structure of a human gammag-immunoglobulin. X. Intrachain disulfid
A:Reference number: A90565; MUID:71064027
A:Contents: annotation; disulfide bonds
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob
enbriome cleavage products, and the disulfide bridges.
A:Reference number: A91667; MUID:77070267
A:Contents: annotation; disulfide bonds
C:Genetics:
A:Gene: GDB:IGHG1
A:Cross-references: GDB:120085; OMTM:147100
A:Map position: 14q32.33-14q32.33
A:Introns: 99/1, 114/1, 224/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into C:Superfamily: immunoglobulin C region; immunoglobulin homology C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin F:20-85/Domain: immunoglobulin homology <IM1> F:137-206/Domain: immunoglobulin homology <IM2> F:243-310/Domain: immunoglobulin homology <IM3> F:27-83,144-204,250-308/Disulfide bonds: #status experimental F:103/Disulfide bonds: interchain (to light chain) #status experimental F:109,112/Disulfide bonds: interchain (to heavy chain) #status experimental F:130/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 54.9%; Score 1233; DB 1; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-71;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKTHTCPPCPAPPELLGSGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
|||||
DB 104 DKTHTCPPCPAPPELLGSGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 163
QY 62 GVEVNAKTRKREDOYNSTYRVSVLYLVHODWLNKGEYKCKVSNKALPAPIETISKAK 121
|||||
DB 164 GVEVNAKTRKREDOYNSTYRVSVLYLVHODWLNKGEYKCKVSNKALPAPIETISKAK 223
QY 122 GQRPPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPNNKTTTPVLD 181
|||||
DB 224 GQRPPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPNNKTTTPVLD 283
QY 182 DGSFELYSKLTVDKSRMOQGNVFCGSVMHEALHNHYTQKSLSISPGK 228
|||||
DB 284 DGSFELYSKLTVDKSRMOQGNVFCGSVMHEALHNHYTQKSLSISPGK 330

RESULT 3
569339
Ig heavy chain V region precursor - human
C:Species: Homo sapiens (man)
C:Dates: 19-Mar-1997 #sequence, revision 19-Mar-1997 #text, change 17-Mar-2000
C:Accession: S69339
R:Khamilich, A.A.; Auncouturier, P.; Preud'homme, J.L.; Cogne, M.
Eur. J. Biochem. 229, 54-60, 1995
A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.
A:Reference number: S69339; MUID:95262687
A:Accession: S69339
A:Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-374 <KHA>
A:Cross-references: EMBL:X81695
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 54.6%; Score 1227; DB 2; Length 374;
Best Local Similarity 99.1%; Pred. No. 3.5e-71;
Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKTHTCPPCPAPPELLGSGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
DB 148 DKTHTCPPCPAPPELLGSGSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNNYVD 207
QY 62 GVEVNAKTRKREDOYNSTYRVSVLYLVHODWLNKGEYKCKVSNKALPAPIETISKAK 121
DB 208 GVEVNAKTRKREDOYNSTYRVSVLYLVHODWLNKGEYKCKVSNKALPAPIETISKAK 267
QY 122 GQRPPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPNNKTTTPVLD 181
DB 268 GQRPPOVYTLPPSRDELTKNOVSLTCLVKGFPYSDIAVEMESNGQEPNNKTTTPVLD 327
QY 182 DGSFELYSKLTVDKSRMOQGNVFCGSVMHEALHNHYTQKSLSISPGK 228
DB 338 DGSFELYSKLTVDKSRMOQGNVFCGSVMHEALHNHYTQKSLSISPGK 374

RESULT 4

S72664

Ig heavy chain V region precursor - human

C:Species: Homo sapiens (man)

C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-2000

C:Accession: S72664

R:Khamlich, A.A. EMBL Data Library, September 1994

Submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X61695

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

Query Match

Best Local Similarity 54.6%; Score 1227; DB 2; Length 374;

Matches 225; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61

148 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 207

62 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121

208 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 267

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 181

268 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 327

182 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

328 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 374

Db 328 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 374

RESULT 5

PT0207

Ig gamma chain C region - chimpanzee

C:Species: Pan troglodytes (chimpanzee)

C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 16-Jul-1999

C:Accession: PT0207

R:Brillich, P.H.; Moustafa, Z.A.; Oestberg, L.

Mol. Immunol. 28: 319-322, 1991

A:Title: Nucleotide sequence of chimpanzee Fc and hinge regions.

A:Reference number: PT0207; MID:91287716

A:Accession: PT0207

Molecule type: mRNA

A:Residues: 1-234 <EHR>

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:48-117/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 52.5%; Score 1180; DB 2; Length 234;

Matches 217; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61

15 DHTHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 74

62 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121

75 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 134

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 181

135 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 194

182 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 221

Db 195 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 234

RESULT 6

A23511

Ig gamma-3 chain C region (allotype G3m(b)) - human

C:Species: Homo sapiens (man)

C:Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 23-Jul-1999

C:Accession: A23511

R:Huck, S.; Fort, P.; Crawford, D.H.; Lefranc, M.P.; Lefranc, G.

Nucleic Acids Res. 14, 1779-1789, 1986

A:Title: Sequence of a human Immunoglobulin gamma 3 heavy chain constant region gene:

A:Reference number: A23511; MID:86148507

A:Accession: A23511

A:Molecule type: DNA

A:Residues: 1-377 <HUC>

A:Cross-references: GB:X03604; GB:M12958; NID:933070; PIDN:CAA27268.1; PID:9577056

C:Genetics:

A:Gene: GDB:IGHG3

A:Cross-references: GDB:119339; OMIM:147120

A:Map position: 14q32.33-14q32.33

A:Insertions: 98/3; 115/3; 130/3; 145/3; 160/3; 270/3

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

F:20-85/Domain: Immunoglobulin homology <IMM>

Query Match

Best Local Similarity 51.0%; Score 1146; DB 2; Length 377;

Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61

151 DTPPCPCPCAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 210

62 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 121

211 GVEVHNNAKTRPREQYSTRVSVLTVLHODMNLNGEKYCKVSNKALPAPIETISKAK 270

122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 181

271 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGQPENNYKTTTPVLDS 330

182 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228

331 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 377

Db 331 DGSFELYSLTLVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 377

RESULT 7

A60764

Ig gamma-3 chain C region, form LAT - human

C:Species: Homo sapiens (man)

C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 16-Jul-1999

C:Accession: A60764

R:Huck, S.; Lefranc, G.; Lefranc, M.P.

Immunogenetics 30, 250-257, 1989

A:Title: A human immunoglobulin IGHG3 allele (Gmb, b1, c3, c5, u) with an IGHG4 con

A:Reference number: A60764; MID:90007613

A:Accession: A60764

A:Status: preliminary

A:Molecule type: DNA

C:Superfamily: Immunoglobulin C region; immunoglobulin homology

C:Keywords: Immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMM>

Query Match

Best Local Similarity 50.9%; Score 1144; DB 2; Length 377;

Matches 210; Conservative 8; Mismatches 9; Indels 0; Gaps 0;

2 DKHTCPCPAPELLGGPSVFLFPPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNMYVD 61

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Db 151 DTPPCPCPCAPBELLGSGSVLEFPKPKDTLMISTPEVTCVVDVSHEDPEVKMYVD 210
QY 62 GVEVNAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAK 121
Db 211 GVEVNAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAK 270
QY 122 GQRPQYVYTLPPSRDELTKNVSLTCLVKGFPSPDIAVEMSNQPENNYKTPPVLD 181
Db 271 GQRPQYVYTLPPSRDELTKNVSLTCLVKGFPSPDIAVEMSNQPENNYKTPPVLD 330
QY 182 DGSFYLTKLVKSRMOGQNFVSCSVMEALHNHYTKSLSPGK 228
Db 331 DGSFYLTKLVKSRMOGQNFVSCSVMEALHNHYTKSLSPGK 377

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RESULT 8

```

G4HU
Species: Homo sapiens (man)
C>Date: 30-Apr-1981 #sequence_revision 13-Jun-1983 #text_change 16-Jul-1999
C/Accession: A93906; A92809; A93132; A02148
R:Ellison, J.; Hood, L.
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982
A>Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con
A/Reference number: A93906; MUID:82197621
A/Accession: A93906
A/Molecule type: DNA
A/Residues: 1-326 <ELL>
A/Note: Lys-326 is probably removed posttranslationally
R:Wang, A.C.; Tung, E.; Fudenberg, H.H.
J. Immunol. 125, 1048-1054, 1980
A>Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f
A/Reference number: A92809; MUID:81007873
A/Contents: myeloma protein t11
A/Accession: A92809
A/Molecule type: Protein
A/Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>
A/Note: Trp-156 is at or near the complement-binding site
R:Connell, G.E.; Parr, D.M.; Hofmann, T.
Can. J. Biochem. 57, 758-767, 1979
A>Title: The amino acid sequences of the three heavy chain constant region domains of a
A/Reference number: A90752; MUID:80001357
A/Contents: myeloma protein z1e
A/Accession: A90752
A/Molecule type: Protein
A/Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-
A/Note: this sequence has since been revised
R:Hofmann, T.; Parr, D.M.
Mol. Immunol. 16, 923-925, 1979
A>Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin g
A/Reference number: A93132; MUID:80114419
A/Contents: z1e
A/Accession: A93132
A/Molecule type: protein
A/Residues: 238-275 <HOF>
R:Hofmann, T.; Parr, D.M.
submitted to the Atlas, March 1980
A/Reference number: A94591
A/Contents: annotation; z1e, revisions to residues 25, 59, 60, and 264-268
A/Note: the revised sequence differs from that shown in having 60-Ala and in the amidat
ned
R:Milstein, C.; Frangione, B.
Biochem. J. 121, 217-225, 1971
A>Title: Disulfide bridges of the heavy chain of human immunoglobulin G2.
A/Reference number: A90253; MUID:72033500
A/Contents: annotation; myeloma protein Sa, disulfide bonds
R:Frangione, B.; Milstein, C.; Pink, J.R.L.
Nature 221, 145-148, 1969
A>Title: Structural studies of immunoglobulin G.
A/Reference number: A93157; MUID:69064124
A/Contents: annotation; Sa, disulfide bonds
C/Genetics:

```

```

A/Gene: GDB:IGHG2
A/Cross-references: GDB:119338; OMIM:147110
A/Map position: 14q32.33-14q32.33
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:135-202/Domain: immunoglobulin homology <IM2>
F:239-306/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 140-200, 246-304/Disulfide bonds: #status experimental
F:102-103, 106-109/Disulfide bonds: interchain (to heavy chain) #status experimental
F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

```

Query Match 50.9%; Score 1142.5; DB 1; Length 326;
Best Local Similarity 94.1%; Pred. No. 7,2e-66;
Matches 209; Conservative 8; Mismatches 4; Indels 1; Gaps 1;

```

```

QY 7 CPGCPAPELGCPVSVEFPKPKDTLMISTPEVTCVVDVSHEDPEVKMYVDGVEVH 66
Db 106 CPGCPAPP-VAGPSVLEFPKPKDTLMISTPEVTCVVDVSHEDPEVQFMVYDGEVH 164
QY 67 NAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAGQPRE 126
Db 165 NAKTRPREQYNSYRVSVLTVLHODMLNGEKCKVSKALPAPIEKTISKAGQPRE 224
QY 127 POYVTLPPSRDELTKNVSLTCLVKGFPSPDIAVEMSNQPENNYKTPPVLDSDGSFF 186
Db 225 POYVTLPPSRDELTKNVSLTCLVKGFPSPDIAVEMSNQPENNYKTPPVLDSDGSFF 284
QY 187 LYSKLTVDKSRMOGQNFVSCSVMEALHNHYTKSLSPGK 228
Db 285 LYSKLTVDKSRMOGQNFVSCSVMEALHNHYTKSLSPGK 326

```

RESULT 9

```

G4HU
Ig gamma-4 chain C region - human
C/Species: Homo sapiens (man)
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 16-Jul-1999
C/Accession: A90933; A90249; A02150
R:Ellison, J.; Buxbaum, J.; Hood, L.
DNA 1, 11-18, 1981
A>Title: Nucleotide sequence of a human immunoglobulin C-gamma4 gene.
A/Reference number: A90933; MUID:83157104
A/Accession: A90933
A/Molecule type: DNA
A/Residues: 1-327 <ELL>
A/Note: the sequence was determined from the germ-line gene
R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.
Biochem. J. 117, 33-47, 1970
A>Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constan
A/Reference number: A90249; MUID:70207560
A/Accession: A90249
A/Molecule type: protein
A/Residues: 1-30; 81-326 <PIN>
C/Genetics:
A/Gene: GDB:IGHG4
A/Cross-references: GDB:119340; OMIM:147130
A/Map position: 14q32.33-14q32.33
A/Introns: 99/1, 111/1, 221/1
C/Complex: An immunoglobulin heterotetramer subunit consists of two identical light (
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into
C/Superfamily: immunoglobulin C region; immunoglobulin homology
C/Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin
F:20-85/Domain: immunoglobulin homology <IM1>
F:99-110/Region: hinge
F:134-203/Domain: immunoglobulin homology <IM2>
F:240-307/Domain: immunoglobulin homology <IM3>
F:14/Disulfide bonds: interchain (to light chain) #status experimental
F:27-83, 141-201, 247-305/Disulfide bonds: #status predicted

```


A: Molecule type: protein
 A: Residues: 129-131,153-172, 'D', 174-184, 'A', 186, 'E', 188-200, 'D', 202-217, 'E', 219-232, 'Q',
 A: Note: This has the e15 allotypic marker, 185-Ala
 C: Complex: An immunoglobulin heterotrimer subunit consists of two identical light (Xp) chain disulfide bonds. In some cases, such as Iga and Igm, the subunits associate into a C: superfamily: immunoglobulin C region; immunoglobulin homology
 C: Keywords: duplication; glycoprotein; heterotrimer; immunoglobulin
 F: 20-82/Domain: immunoglobulin homology <IM1>
 F: 130-199/Domain: immunoglobulin homology <IM2>
 F: 236-303/Domain: immunoglobulin homology <IM3>
 F: 173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 40.9%; Score 918.5; DB 1; Length 323;
 Best Local Similarity 71.7%; Pred. No. 1.3e-51;
 Matches 167; Conservative 29; Mismatches 32; Indels 5; Gaps 2;

1 MDKT---HTC--PPCPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
 91 VDKVAVSTGSKPTCPPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSDGDEPEVQ 150
 56 FNNVVDGEVHNAKTKPREEOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEK 115
 131 FTWYINNEQVYRTARPPLEQGFNSTIRVSTLPITHDWLNGKEFKCKVHNKALPAPIEK 210
 116 TISAKAGQPEPOVYITLPSPDELTKNQVSTLCVKGFPSPDIAMWESNQPPENNYKTT 175
 211 TISAKAGQPEPOVYITLPSPDELTKNQVSTLCVKGFPSPDIAMWESNQPPENNYKTT 270
 176 PPVVDGSGSEFLYKTLVDKSRMVGQVFCSCVMHEALHNHYTKSLSPGK 228
 271 PAVLDSGSGSEFLYKTLVDKSRMVGQVFCSCVMHEALHNHYTKSLSPGK 323

RESULT 12

147160

Ig gamma 2b chain constant region - pig (fragment)

C: Species: Sus scrofa domestica (domestic pig)
 C: Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C: Accession: I47160

R: Raskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A: Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A: Reference number: I47158; MUID: 95015845

A: Accession: I47160

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-328 <KAC>

A: Cross-references: EMBL:U03780; NID: g433125; PIDN: AAA52218.1; PID: g433126

C: Superfamily: Immunoglobulin C region; immunoglobulin homology

F: 133-202/Domain: immunoglobulin homology <IM1>

Query Match 40.4%; Score 906.5; DB 2; Length 328;
 Best Local Similarity 73.2%; Pred. No. 7.5e-51;
 Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

7 CPPPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVH 66
 106 CPICPACE-SGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVH 164
 67 NAKTKPREEOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISSAKAGQPRE 126
 165 TAQTRPREEOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISSAKAGQPRE 224
 127 PÖYVTLPPSDELTKNQVSTLCVKGFPSPDIAMWESNQ--PENNYKTTPPVLDSGDS 184
 225 PÖYVTLPPSDELTKNQVSTLCVKGFPSPDIAMWESNQ--PENNYKTTPPVLDSGDS 284
 185 FFYLSKLTVDKSRMVGQVFCSCVMHEALHNHYTKSLSPGK 228

DB 285 YFLSKFSVDKASMOGGGIRQCAVMHEALHNHYTKSLSPGK 328

RESULT 13

147159

Ig gamma 2a chain constant region - pig (fragment)

C: Species: Sus scrofa domestica (domestic pig)
 C: Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C: Accession: I47159

R: Raskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A: Title: Five putative subclasses of swine IgG identified from the cDNA sequences of

A: Reference number: I47158; MUID: 95015845

A: Accession: I47159

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Residues: 1-328 <KAC>

A: Cross-references: EMBL:U03779; NID: g433123; PIDN: AAA52217.1; PID: g433124

C: Superfamily: Immunoglobulin C region; immunoglobulin homology

F: 133-202/Domain: immunoglobulin homology <IM1>

Query Match 40.4%; Score 906.5; DB 2; Length 328;
 Best Local Similarity 73.2%; Pred. No. 7.5e-51;
 Matches 164; Conservative 29; Mismatches 28; Indels 3; Gaps 2;

7 CPPPABELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVH 66
 106 CPICPACE-SGPGSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNNVYDGEVH 164
 67 NAKTKPREEOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISSAKAGQPRE 126
 165 TAQTRPREEOYNSTYRVSVLTVLHODWLNKGEYKCKVSNKALPAPIEKTISSAKAGQPRE 224
 127 PÖYVTLPPSDELTKNQVSTLCVKGFPSPDIAMWESNQ--PENNYKTTPPVLDSGDS 184
 225 PÖYVTLPPSDELTKNQVSTLCVKGFPSPDIAMWESNQ--PENNYKTTPPVLDSGDS 284
 185 FFYLSKLTVDKSRMVGQVFCSCVMHEALHNHYTKSLSPGK 228
 285 YFLSKFSVDKASMOGGGIRQCAVMHEALHNHYTKSLSPGK 328

RESULT 14

147162

Ig gamma 4 chain constant region - pig (fragment)

C: Species: Sus scrofa domestica (domestic pig)
 C: Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000

C: Accession: I47162

R: Raskovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A: Title: Five putative subclasses of swine IgG identified from the cDNA sequences of

A: Reference number: I47158; MUID: 95015845

A: Accession: I47162

A: Status: preliminary; translated from GB/EMBL/DBJ

A: Molecule type: mRNA

A: Cross-references: EMBL:U03782; NID: g433129; PIDN: AAA52220.1; PID: g433130

C: Superfamily: Immunoglobulin C region; immunoglobulin homology

F: 82-151/Domain: immunoglobulin homology <IM1>

Query Match 40.2%; Score 903.5; DB 2; Length 277;
 Best Local Similarity 71.1%; Pred. No. 9.6e-51;
 Matches 167; Conservative 30; Mismatches 31; Indels 7; Gaps 4;

1 MDK---HTCPCP-ABELLG-SPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 55
 43 VDKVAVSTGSKPTCPPELLGSPVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVK 102

QY 56 FNNYVDCGEVHNKAKTREREOYNSTRVSVLYLVHODWLNKGEYCKCKVSNKALPAPIEK 115
 DB 103 FSNVVDCEVHTAQTORPEKEOFNSTRVSVLYLVHODWLNKGEYCKCKVSNKALPAPIETR 162
 QY 116 TISKACQPEPPQVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNGQ--PENNYK 173
 DB 163 TISKACQPEPPQVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNGQPEEGNYR 222
 QY 174 TTPVLDSGSEFFLYSKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPGK 228
 DB 223 TTPQGVDDGYFFLYSKLAVDKASMGNDTFQCAVMHEALHNHYTOKSLSPGK 277

RESULT 15

G2GP

Ig gamma-2 chain C region - guinea pig

C:Species: Cavia porcellus (guinea pig)

C:Date: 07-May-1981 #sequence_revision 07-May-1981 #text_change 16-Jul-1999

C:Accession: A94553; A90352; A90359; A90384; A90385; A02151

C:Submitted to the Atlas, April 1975

A:Reference number: A94553

A:Molecule type: protein

A:Residues: 1-3 <TR>

R:Birthstein, B.K.; Hussain, Q.Z.; Cebra, J.J.

Biochemistry 10, 18-25, 1971

A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ant

A:Reference number: A90352

A:Molecule type: protein

A:Residues: 4-68 <BI>

R:Turner, K.J.; Cebra, J.J.

Biochemistry 10, 9-17, 1971

A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). II. Ant

A:Reference number: A90359; MUID:71058486

A:Accession: A90359

A:Molecule type: protein

A:Residues: 69-133;312-329 <TR>

R:Tracey, D.E.; Cebra, J.J.

Biochemistry 13, 4796-4803, 1974

A:Title: Primary structure of the C-H2 homology region from guinea pig IgG2 antibodies.

A:Reference number: A90384; MUID:75056072

A:Accession: A90384

A:Molecule type: protein

A:Residues: 134-226 <TR>

R:Trischmann, T.M.; Cebra, J.J.

Biochemistry 13, 4804-4811, 1974

A:Title: Primary structure of the C-H3 homology region from guinea pig IgG2 antibodies.

A:Reference number: A90385; MUID:75056073

A:Accession: A90385

A:Molecule type: protein

A:Residues: 227-311 <TR>

R:Oliveira, B.; Lamm, M.E.

Biochemistry 10, 26-31, 1971

A:Title: Interchain disulfide bridges of guinea pig gamma-2- immunoglobulin.

A:Reference number: A90354; MUID:71058474

A:Contents: annotation; disulfide bonds

A:Note: Cys-16 is involved in a heavy-light chain bond

C:Comment: This chain was isolated from pooled serum of strain 13 inbred guinea pigs.

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

ha) disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 16

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:21-81/Domain: immunoglobulin homology <IM1>

F:135-204/Domain: immunoglobulin homology <IM2>

F:241-310/Domain: immunoglobulin homology <IM3>

F:28-79/Disulfide bonds: #status experimental

F:142-202/Disulfide bonds: #status experimental

F:178/Binding site: carbohydrate (Asn) (covalent) #status experimental

F:248-308/Disulfide bonds: #status experimental

Query Match 39.6%; Score 889; DB 1; Length 329;
 Best Local Similarity 72.3%; Pred. No. 9, 7e-50;
 Matches 162; Conservative 24; Mismatches 36; Indels 2; Gaps 1;

QY 6 TCPPCPAPPELLGSPVFLFPKPKDLMISRTPEYTCVVVDVSHEDPEVFNNYVDCGEV 65
 DB 106 TCPPCPAPPELLGSPVFLFPKPKDLMISRTPEYTCVVVDVSHEDPEVFNNYVDCGEV 165
 QY 66 HNAKTREREOYNSTRVSVLYLVHODWLNKGEYCKCKVSNKALPAPIEKTISKAKQPR 125
 DB 166 GNAETKPRVQINTTFRVESVLPQIHDWLNKGEYCKCKVSNKALPAPIEKTISKAKQPR 225
 QY 126 EPOVYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNGQ--ENNYYTTPVLDSG 183
 DB 226 MPDVTYTLPPSRDELTKNOVSLTCLVKGYPSPDIAVEMESNGQ--ENNYYTTPVLDSG 285
 QY 184 SFPLYSKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPGK 227
 DB 286 SFPLYSKLTVDKSRMOGNFSCSVMEALHNHYTOKSLSPGK 329

Search completed: December 27, 2000, 10:54:40
 Job time: 191 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:56 ; Search time 27.53 Seconds
(without alignments)
244.142 Million cell updates/sec

Title: US-09-389-545-8

2246

Perfect score: 1 MDKHTCPCPAPPELLGSPS.....QKGNATHNIGSGNSESTOK 401

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 164575 seqs, 16761186 residues

al number of hits satisfying chosen parameters: 164575

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/1aa/5A_COMB.pep.*
- 2: /cgn2_6/ptodata/2/1aa/5B_COMB.pep.*
- 3: /cgn2_6/ptodata/2/1aa/6_COMB.pep.*
- 4: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep.*
- 5: /cgn2_6/ptodata/2/1aa/Packfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1234	54.9	347	1	US-07-940-861-43 Sequence 43, Appl
2	1234	54.9	347	1	US-08-459-512-43 Sequence 43, Appl
3	1234	54.9	347	2	US-08-459-657-43 Sequence 43, Appl
4	1234	54.9	347	2	US-08-460-132-43 Sequence 43, Appl
5	1234	54.9	347	4	PCT-US92-02050-43 Sequence 43, Appl
6	1233	54.9	323	2	US-08-595-043A-50 Sequence 50, Appl
7	1233	54.9	371	1	US-08-236-311-7 Sequence 7, Appl
8	1233	54.9	371	3	US-08-457-918-7 Sequence 7, Appl
9	1233	54.9	387	1	US-08-470-299-4 Sequence 4, Appl
10	1233	54.9	396	2	US-08-784-512-3 Sequence 3, Appl
11	1233	54.9	424	4	PCT-US95-03866-12 Sequence 12, Appl
12	1233	54.9	424	4	PCT-US95-03866-14 Sequence 14, Appl
13	1233	54.9	437	4	PCT-US96-10043-11 Sequence 11, Appl
14	1233	54.9	442	4	PCT-US96-10043-9 Sequence 9, Appl
15	1233	54.9	449	1	US-08-458-516-13 Sequence 13, Appl
16	1233	54.9	459	1	US-08-157-101A-7 Sequence 7, Appl
17	1233	54.9	476	2	US-08-378-939-10 Sequence 10, Appl
18	1233	54.9	476	3	US-08-487-550-4 Sequence 4, Appl
19	1233	54.9	476	3	US-08-487-550-12 Sequence 12, Appl
20	1233	54.9	476	3	US-08-487-550-8 Sequence 8, Appl
21	1238	54.7	254	2	US-08-284-391B-33 Sequence 33, Appl
22	1228	54.7	664	3	US-08-957-063-16 Sequence 16, Appl
23	1228	54.7	664	3	US-08-957-063-18 Sequence 18, Appl
24	1227	54.6	449	3	US-08-897-236-23 Sequence 23, Appl
25	1227	54.6	451	2	US-08-887-352B-14 Sequence 14, Appl
26	1227	54.6	451	2	US-08-887-352B-16 Sequence 16, Appl
27	1227	54.6	451	2	US-08-887-352B-18 Sequence 18, Appl
28	1227	54.6	451	3	US-08-466-151-65 Sequence 65, Appl

29	1227	54.6	452	3	US-09-027-449-71 Sequence 71, Appl
30	1227	54.6	453	3	US-08-466-151-8 Sequence 8, Appl
31	1227	54.6	454	2	US-07-934-373C-22 Sequence 22, Appl
32	1227	54.6	454	3	US-08-437-642B-22 Sequence 22, Appl
33	1224	54.6	454	4	PCT-US93-07832-22 Sequence 22, Appl
34	1224	54.5	911	2	US-08-484-438-10 Sequence 10, Appl
35	1221	54.4	442	1	US-08-461-968A-5 Sequence 5, Appl
36	1221	54.4	442	2	US-08-462-571-5 Sequence 5, Appl
37	1216.5	54.2	486	1	US-08-243-010-1 Sequence 1, Appl
38	1216.5	54.2	552	1	US-08-243-010-6 Sequence 6, Appl
39	1215	54.1	438	1	US-06-097-827-11 Sequence 11, Appl
40	1215	54.1	438	1	US-08-494-574-11 Sequence 11, Appl
41	1212	54.0	232	1	US-07-797-556-4 Sequence 4, Appl
42	1212	54.0	232	1	US-08-225-989-4 Sequence 4, Appl
43	1212	54.0	232	1	US-08-570-923-4 Sequence 4, Appl
44	1212	54.0	232	1	US-08-580-014-4 Sequence 4, Appl
45	1212	54.0	232	4	PCT-US95-06530-4 Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-07-940-861-43
; Sequence 43, Application US/07940861
; Patent No. 5547853
; GENERAL INFORMATION:
; APPLICANT: BIOGEN, INC.
; APPLICANT: WALLNER, Barbara P.
; APPLICANT: MILLER, Glenn T.
; APPLICANT: ROSA, Margaret D.
; TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
; TITLE OF INVENTION: FUNCTION ASSOCIATED ANTIGEN 3
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Neave
; STREET: 875 Third Avenue
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10022-6250
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07940,861
; FILING DATE: 21-OCT-1992
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/02050
; FILING DATE: 12-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/667,971
; FILING DATE: 12-MAR-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/770,967
; FILING DATE: 07-OCT-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: HALEY, James F., Jr.
; REGISTRATION NUMBER: 27,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)715-0600
; TELEFAX: (212)715-0673
; TELETYPE: 14-8367
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 347 amino acids
; TYPE: amino acids
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-07-940-861-43

Query Match 54.9%; Score 1234; DB 1; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDPEVKFNMY 60
DB 120 VDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDPEVKFNMY 179
QY 61 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 120
DB 180 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 239
QY 121 KQGPPEQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLD 180
DB 240 KQGPPEQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLD 299
181 SDGSFELYSKLTVDKSRMOGQNFVSCVMHEALHNHYTKSLSPGK 228
DB 300 SDGSFELYSKLTVDKSRMOGQNFVSCVMHEALHNHYTKSLSPGK 347

RESULT 2
US-08-459-512-43

Sequence 43, Application US/08459512
Patent No. 5728677
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: MILLER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,512
FILING DATE: 02-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15ICIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-459-512-43

Query Match 54.9%; Score 1234; DB 1; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDPEVKFNMY 60
DB 120 VDKHTPCPCAPAPLGGPSVFLFPKPKDTLMSRTEPYTCVYVDVSHDPEVKFNMY 179
QY 61 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 120
DB 180 DGEVHNKAKTRPEQYNSYTRVSVLTVLHODMLNGEKYCKVSNKALPAPIETISKA 239
QY 121 KQGPPEQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLD 180
DB 240 KQGPPEQVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEMESNGOPENNYKTPPVLD 299
181 SDGSFELYSKLTVDKSRMOGQNFVSCVMHEALHNHYTKSLSPGK 228
DB 300 SDGSFELYSKLTVDKSRMOGQNFVSCVMHEALHNHYTKSLSPGK 347

RESULT 3
US-08-459-657-43

Sequence 43, Application US/08459657
Patent No. 5914111
GENERAL INFORMATION:
APPLICANT: BIOGEN, INC.
APPLICANT: MILLER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,657
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B15ICIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-459-657-43

Query Match 54.9%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEKFNWY 60
DB 120 VDKTHCPAPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEKFNWY 179
QY 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODMLNGEKYCKVSKALPALEKITSKA 120
DB 180 DGEVHNAKTRPREQYNSTRVSVLTVLHODMLNGEKYCKVSKALPALEKITSKA 239
QY 121 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGPENNYKTPPVLD 180
DB 240 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGPENNYKTPPVLD 299
181 SDGSFLYSKLTVDKSRMOQGNFSCSVMHDLNHNHTOKSLSPGK 228
DB 300 SDGSFLYSKLTVDKSRMOQGNFSCSVMHDLNHNHTOKSLSPGK 347

RESULT 4
US-08-460-132-43
Sequence 43, Application US/08460132
Patent No. 5928643

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460,132
FILING DATE: 02-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/940,861
FILING DATE: 21-OCT-1992
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 12-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367

INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 347 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-460-132-43

Query Match 54.9%; Score 1234; DB 2; Length 347;
Best Local Similarity 99.6%; Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHCPAPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEKFNWY 60
DB 120 VDKTHCPAPAPELLGGPSVFLFPKPKDTLMISRTPEVTCVVDVSHDEPEKFNWY 179
QY 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODMLNGEKYCKVSKALPALEKITSKA 120
DB 180 DGEVHNAKTRPREQYNSTRVSVLTVLHODMLNGEKYCKVSKALPALEKITSKA 239
QY 121 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGPENNYKTPPVLD 180
DB 240 KGPPEQVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWEMESNGPENNYKTPPVLD 299
181 SDGSFLYSKLTVDKSRMOQGNFSCSVMHDLNHNHTOKSLSPGK 228
DB 300 SDGSFLYSKLTVDKSRMOQGNFSCSVMHDLNHNHTOKSLSPGK 347

RESULT 5
PCT-US92-02050-43

Sequence 43, Application PC/TUS9202050

GENERAL INFORMATION:

APPLICANT: BIOGEN, INC.
APPLICANT: WALLNER, Barbara P.
APPLICANT: MILLER, Glenn T.
APPLICANT: ROSA, Margaret D.
TITLE OF INVENTION: CD2-BINDING DOMAIN OF LYMPHOCYTE
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Neave
STREET: 875 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022-6250
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/02050
FILING DATE: 19920312
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/667,971
FILING DATE: 12-MAR-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/770,967
FILING DATE: 07-OCT-1991
ATTORNEY/AGENT INFORMATION:
NAME: HALEY, James F., Jr.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: B151CIP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)715-0600
TELEFAX: (212)715-0673
TELEX: 14-8367
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:

LENGTH: 347 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-02050-43

Query Match 54.9%: Score 1234; DB 4; Length 347;
Best Local Similarity 99.6%: Pred. No. 1.2e-97;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MDKTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNMYV 60
Db 120 VDKTTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNMYV 179
Qy 61 DGEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 120
Db 180 DGEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 239
Qy 121 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNKKTPPVLD 180
Db 240 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNKKTPPVLD 299
Qy 181 SDGSFLLSKLTVDSKRMQGNVFCSVMHKALHNHYTQKSLSLSPGK 228
Db 300 SDGSFLLSKLTVDSKRMQGNVFCSVMHKALHNHYTQKSLSLSPGK 299

RESULT 6
US-08-595-043A-50
Sequence 50, Application US/08595043A
Patent No. 5935824
GENERAL INFORMATION:
APPLICANT: SGARLATO, GREGORY D.
TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
NUMBER OF SEQUENCES: 90
CORRESPONDENCE ADDRESS:
ADDRESSEE: MEDLEN & CARROLL
STREET: 220 MONTGOMERY STREET, SUITE 2200
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,043A
FILING DATE: 31-JAN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: CARROLL, PETER G.
REGISTRATION NUMBER: 32,837
REFERENCE/DOCKET NUMBER: SGAR-00371
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 705-8410
TELEFAX: (415) 397-8338
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-043A-50

Query Match 54.9%: Score 1233; DB 2; Length 232;
Best Local Similarity 100.0%: Pred. No. 8.3e-86;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNMYV 61

Db 6 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVAVDVSHEDPEVKFNMYV 65
Qy 62 GVEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 121
Db 66 GVEVHNNAKTRPEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAK 125
Qy 122 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNKKTPPVLD 181
Db 126 GQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESGOPENNKKTPPVLD 185
Qy 182 DGSFLLSKLTVDSKRMQGNVFCSVMHKALHNHYTQKSLSLSPGK 228
Db 186 DGSFLLSKLTVDSKRMQGNVFCSVMHKALHNHYTQKSLSLSPGK 232

RESULT 7
US-08-236-311-7
Sequence 7, Application US/08236311
Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/2250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-1896
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-236-311-7

Query Match 54.9%: Score 1233; DB 1; Length 371;
Best Local Similarity 100.0%: Pred. No. 1.6e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 145 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 204
QY 62 GVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
Db 205 GVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 264
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 324
QY 182 DGSFELSKLTVDKSRWQGQVNFSCSYMHDLNHNHTOKSLSPGK 228
Db 325 DGSFELSKLTVDKSRWQGQVNFSCSYMHDLNHNHTOKSLSPGK 371

RESULT 8

US-08-457-918-7
Sequence 7, Application US/08457918
Patent No. 6117635

GENERAL INFORMATION:

APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adhesion Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 Inch, 360 Kb floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/457, 918
FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/2250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104323
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kudinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELEPHONE: 415/225-8228
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-457-918-7

Query Match 54.9%; Score 1233; DB 3; Length 371;
Best Local Similarity 100.0%; Pred. No. 1.6e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 145 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 204
QY 62 GVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 121
Db 205 GVEVHNKATKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTISKAK 264
QY 122 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 181
Db 265 GQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLD 324
QY 182 DGSFELSKLTVDKSRWQGQVNFSCSYMHDLNHNHTOKSLSPGK 228
Db 325 DGSFELSKLTVDKSRWQGQVNFSCSYMHDLNHNHTOKSLSPGK 371

RESULT 9

US-08-470-299-4
Sequence 4, Application US/08470299
Patent No. 5783181

GENERAL INFORMATION:

APPLICANT: Browne, Michael J.
APPLICANT: Murphy, Kay E.
APPLICANT: Chapman, Conrad G.
APPLICANT: Clinkbeard, Helen E.
APPLICANT: Young, Peter R.
APPLICANT: Shatzman, Allan R.
TITLE OF INVENTION: No. 5783181el Compounds
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road, P.O. Box 1539
CITY: King of Prussia
STATE: Pennsylvania
COUNTRY: USA
ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,299
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Sutton, Jeffrey A.
REGISTRATION NUMBER: 34,028
REFERENCE/DOCKET NUMBER: P31005C3
TELEPHONE: 610-270-5024
TELEFAX: 610-270-5090
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 387 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-470-299-4

Query Match 54.9%; Score 1233; DB 1; Length 387;
Best Local Similarity 100.0%; Pred. No. 1.7e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 61
Db 161 DKHTCPPCAPAPLLGGPSVFLFPPKPKDILMISRTPEVTCVVVDVSHEDPEVKFNNYVD 220

QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 221 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 280
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQPENNKTTTPVLD 181
DB 281 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQPENNKTTTPVLD 340
QY 182 DGSFFLYSKLTVDKSRMOQGNVFCGVMHEALHNHYTKSLSPGK 228
DB 341 DGSFFLYSKLTVDKSRMOQGNVFCGVMHEALHNHYTKSLSPGK 387

RESULT 10
US-08-784-512-3

; Sequence 3, Application US/08784512
; Patent No. 5872209
; GENERAL INFORMATION:
; APPLICANT: BARTNIK, Eckart
; APPLICANT: EIDENMUELLER, Bernd
; APPLICANT: BOETTNER, Frank
; APPLICANT: CATERSON, Bruce
; APPLICANT: HUGHES, Clare
; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)
; TITLE OF INVENTION: and native aggregan to study the proteolytic activity of
; TITLE OF INVENTION: "aggreganase" in cell culture systems
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: Suite 500, 3000 K Street, N.W.
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/784,512
; FILING DATE: 17-JAN-1997
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 96100682.2
; FILING DATE: 18-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: GRANADOS, Patricia D.
; REFERENCE/DOCKET NUMBER: 33,683
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202)672-5300
; TELEFAX: (202)672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..396
; US-08-784-512-3

Query Match 54.9%; Score 1233; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 1,7e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 61
DB 170 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 229

QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 230 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 289
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQPENNKTTTPVLD 181
DB 290 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQPENNKTTTPVLD 349
QY 182 DGSFFLYSKLTVDKSRMOQGNVFCGVMHEALHNHYTKSLSPGK 228
DB 350 DGSFFLYSKLTVDKSRMOQGNVFCGVMHEALHNHYTKSLSPGK 396

RESULT 11
PCT-US95-03866-12

; Sequence 12, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: Cytomed, Inc. (all states except US)
; APPLICANT: Nocke, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994;
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F.
; REFERENCE/DOCKET NUMBER: 27,794
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9090
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 12:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; PCT-US95-03866-12

Query Match 54.9%; Score 1233; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.9e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 61
DB 198 DKHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNMYVD 257
QY 62 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 121
DB 258 GVEYHNATKREBOYNSTYRVSVLTVLHODMLNGKEYCKVSNKALPAPIEKTISKAK 317
QY 122 GQREPOVYTLPPSRDELTKNOVSLTCLVKGFPSPDIWENESNGQPENNKTTTPVLD 181

DB 318 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNKTTPVLDS 377
QY 182 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 378 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 424

RESULT 12

PCT-US95-03866-14
; Sequence 14, Application PC/TUS9503866
; GENERAL INFORMATION:
; APPLICANT: CytoMed, Inc. (all states except US)
; APPLICANT: Nocke, Karl (US only)
; APPLICANT: Lobell, Robert B (US only)
; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND
; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND
; NUMBER OF SEQUENCES: 36
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States of America
; ZIP: 10020
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/03866
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/220,379
; FILING DATE: 28-MAR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Haley Jr, James F
; REGISTRATION NUMBER: 27,794
; REFERENCE/DOCKET NUMBER: CytoMed/2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-596-9000
; TELEFAX: 212-596-9090
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 424 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
-US95-03866-14

Query Match 54.9%; Score 1233; DB 4; Length 424;
Best Local Similarity 100.0%; Pred. No. 1.9e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFMYYVD 61
DB 198 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFMYYVD 257
QY 62 GGVVHNAKTRPREOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTTISKAK 121
DB 258 GGVVHNAKTRPREOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTTISKAK 317
QY 122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNKTTPVLDS 181
DB 318 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNKTTPVLDS 377
QY 182 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 378 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 424

RESULT 13

PCT-US96-10043-11
; Sequence 11, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES
; TITLE OF INVENTION: AND METHODS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02210-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/10043
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/000,213
; FILING DATE: 14-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lech, Karen F.
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 00786/284001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-10043-11

Query Match 54.9%; Score 1233; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFMYYVD 61
DB 211 DKHTGCPAPAPLLGGPSVFLPPPKKDTLMSRTPEVTCVVVDVSHEDPEVKFMYYVD 270
QY 62 GGVVHNAKTRPREOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTTISKAK 121
DB 271 GGVVHNAKTRPREOYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKTTISKAK 330
QY 122 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNKTTPVLDS 181
DB 331 GQREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGOPENNKTTPVLDS 390
QY 182 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 228
DB 391 DGSFELYSLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPGK 437

RESULT 14

PCT-US96-10043-9
; Sequence 9, Application PC/TUS9610043
; GENERAL INFORMATION:
; APPLICANT: The General Hospital Corporation
; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

TITLE OF INVENTION: AND METHODS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02210-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/10043
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/000,213
FILING DATE: 14-JUN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lech, Karen F.
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 00786/284001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 442 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-10043-9

Query Match 54.9%; Score 1233; DB 4; Length 442;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPPCPAPELLGSGSVFLPPKPKDMLTMRPEVTCVVVDVSHEDPEVKFNNYVD 61
DB 216 DKHTCPPCPAPELLGSGSVFLPPKPKDMLTMRPEVTCVVVDVSHEDPEVKFNNYVD 275
QY 62 GVEVHNNAKTRPREQYNSYTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKAK 121
DB 276 GVEVHNNAKTRPREQYNSYTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKAK 335
QY 122 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
DB 336 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 395
QY 182 DGSFELYSKLTVDKSRMQGVNFCVSMHEALHNHYTQKSLSLSPGK 228
DB 396 DGSFELYSKLTVDKSRMQGVNFCVSMHEALHNHYTQKSLSLSPGK 442

RESULT 15
US-08-458-516-13
Sequence 13, Application US/08458516
Patent No. 5777085
GENERAL INFORMATION:
APPLICANT: CO, Man Sung
APPLICANT: Tso, J. Yun
TITLE OF INVENTION: Humanized Antibodies Reactive with
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: William M. Smith

STREET: One Market Plaza, Stewart Tower, Suite 2000
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/458,516
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/059,159
FILING DATE: 03-MAY-1993
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11823-37-3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-326-2400
TELEFAX: 415-326-2422
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 449 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-458-516-13

Query Match 54.9%; Score 1233; DB 1; Length 449;
Best Local Similarity 100.0%; Pred. No. 2e-97;
Matches 227; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2 DKHTCPPCPAPELLGSGSVFLPPKPKDMLTMRPEVTCVVVDVSHEDPEVKFNNYVD 61
DB 223 DKHTCPPCPAPELLGSGSVFLPPKPKDMLTMRPEVTCVVVDVSHEDPEVKFNNYVD 282
QY 62 GVEVHNNAKTRPREQYNSYTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKAK 121
DB 283 GVEVHNNAKTRPREQYNSYTRVSVLTVLHODWLNKREYCKVSNKALPAPIETISKAK 342
QY 122 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 181
DB 343 GQPREPOVYLLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 402
QY 182 DGSFELYSKLTVDKSRMQGVNFCVSMHEALHNHYTQKSLSLSPGK 228
DB 403 DGSFELYSKLTVDKSRMQGVNFCVSMHEALHNHYTQKSLSLSPGK 449

Search completed: December 27, 2000, 10:53:58
Job time: 149 sec

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GenCore version 4.5
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OM protein - protein search, using sw model

Run on: December 27, 2000, 10:53:25 ; Search time 40.04 Seconds

(without alignments)
342,450 Million cell updates/sec

Title: US-09-389-545-8

Perfect score: 2246

Sequence: 1 MDKHTCCPPCAPPELLGGPS.....QKGNATHDNICGSESTQK 401

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 268485 seqs, 34193795 residues

Minimum number of hits satisfying chosen parameters: 268485

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

A.GeneSeq.36.*
1: /SIDSL/gcgdata/geneseq/geneseq/AA1980.DAT.*
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15: /SIDSL/gcgdata/geneseq/geneseq/AA1994.DAT.*
16: /SIDSL/gcgdata/geneseq/geneseq/AA1995.DAT.*
17: /SIDSL/gcgdata/geneseq/geneseq/AA1996.DAT.*
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21: /SIDSL/gcgdata/geneseq/geneseq/AA2000.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1239.5	55.2	652	19 W48650	Heavy chain of hmb
2	1238	55.1	374	19 W83963	Recombinant human
3	1238	55.1	374	19 W49075	Recombinant human
4	1237	55.1	235	20 Y01372	Amino acid sequenc
5	1236.5	55.1	651	18 W26649	Chimeric receptor
6	1236.5	55.1	692	18 W26650	Chimeric receptor
7	1234	54.9	347	13 R27163	CD2 binding LFA-3-
8	1234	54.9	347	21 Y83136	Human Transmembran
9	1234	54.9	388	19 W73513	Rabbit TGFbetaRII:
10	1234	54.9	388	19 W73514	Human TGFbetaRII:
11	1234	54.9	388	21 Y54063	Amino acid sequenc
12	1234	54.9	388	21 Y54064	Amino acid sequenc

13	1234	54.9	399	21 Y70867	Human interferon-b
14	1234	54.9	418	21 Y70868	Human interferon-b
15	1234	54.9	423	21 Y70869	Human interferon-b
16	1234	54.9	446	15 R58753	VCAM 2D-IgG. Homo
17	1234	54.9	446	20 Y23986	VCAM 2D-IgG, a sol
18	1234	54.9	446	20 Y01037	VCAM 2D-IgG protei
19	1234	54.9	446	20 W96743	A VCAM 2D-IgG fus
20	1234	54.9	482	19 W31646	Human cytokine rec
21	1233	54.9	232	18 W26232	Human IgG1 hinge/F
22	1233	54.9	233	20 Y06617	Human Fc (IgG1).
23	1233	54.9	259	20 Y24154	Protein from pCd51
24	1233	54.9	329	17 R91806	Human immunoglobul
25	1233	54.9	351	14 R43685	Human kappa immuno
26	1233	54.9	371	10 P91918	Sequence of the li
27	1233	54.9	371	10 P93558	Linkered human IgG
28	1233	54.9	376	19 W60037	Antigenic peptide
29	1233	54.9	379	19 W83962	Recombinant human
30	1233	54.9	379	19 W49073	Recombinant human
31	1233	54.9	379	19 W49074	Recombinant human
32	1233	54.9	387	17 R90920	IL4.Y124D/IgG1 pro
33	1233	54.9	396	18 W18574	Aggrecanase artifi
34	1233	54.9	396	18 W18575	Aggrecanase artifi
35	1233	54.9	400	21 Y15123	Porcine CTLA-4-Ig
36	1233	54.9	424	16 W14764	Human soluble kit
37	1233	54.9	424	16 W14765	Human soluble kit
38	1233	54.9	435	13 R26530	Sequence of one ch
39	1233	54.9	437	18 W10552	Alpha-1-acid glyco
40	1233	54.9	442	18 W10550	IgG1 polypeptide.
41	1233	54.9	445	20 Y24153	Bovine Ix-1 extra
42	1233	54.9	446	17 W05829	Humanised Id10 ant
43	1233	54.9	447	20 Y31659	Human IgG1 chain C
44	1233	54.9	449	14 R43339	Completely humanis
45	1233	54.9	449	19 W49816	Amino acid sequenc

ALIGNMENTS

RESULT	1	
W48650	W48650 standard; Protein; 652 AA.	
XX	XX	
AC	W48650;	
XX	XX	
DT	04-AUG-1998 (first entry)	
XX	XX	
DE	Heavy chain of hmb425 fused to TNF alpha.	
XX	XX	
KW	Antibody-cytokine fusion protein; tricomplex vector; chimeric; TNF alpha; IL-2; IRES; Internal ribosome entry site.	
XX	XX	
OS	Synthetic.	
OS	Homo sapiens.	
XX	XX	
FT	Key	Location/Qualifiers
FT	Region	1..494
FT	Region	/note= "Heavy chain of human mab 425"
FT	Region	495..652
FT	Region	/note= "TNF alpha"
PN	W09811241-A1.	
XX	XX	
PD	19-MAR-1998.	
XX	XX	
PF	02-SEP-1997; 97WO-EP04765.	
XX	XX	
PR	30-SEP-1996; 96EP-0115635.	
PR	16-SEP-1996; 96EP-0114820.	
XX	XX	
PA	(MERE) MERCK PATENT GMBH.	
PI	Brummer W, Burge C, Dunker R, Hauser H, Mielke C; Rieke E, Von Hoegen I, Welge T;	

XX WPI: 1998-207400/18.
DR N-PSDB; V18096.
XX
PT Oligo/cistronic expression vector - useful for production of, e.g.
XX MAb425/TNF- α or MAb425/IL-2 antibody fusion protein
XX
PS Disclosure: Fig 15; 89pp; English.
XX
CC The present sequence represents a fusion protein comprising of TNF
CC alpha fused to the C-terminus of the heavy chain of the human
CC monoclonal antibody 425 (hmb425). The hmb425 has specificity for
CC the human EGF receptor. The invention claims for a new pMCDDHAP
CC tricistronic vector (V18096) for the expression of an antibody-cytokine
CC fusion protein, hmb425-TNF alpha. The TNF alpha sequence can be
CC substituted by the IL-2 sequence. The vector also contains a strong
CC promoter/enhancer unit, a selection marker gene and at least two
CC poliovirus derived internal ribosomal entry site (IRES) sequences. The
CC hetero can be expressed in mammalian host cells for the production of
XX heteromeric fusion proteins. This expression system is claimed to
XX produce the heteromeric proteins in high yields.

Query Match	55.2%	Score 1239.5	DB 19	Length 652
Best Local Similarity	65.8%	Pred NO. 9.4e-76		
Matches 250	Conservative 19	Mismatches 54	Indels 57	Gaps 6

[illegible]

RESULT	2
W83963	
ID	W83963 standard; Protein; 374 AA.
XX	
AC	W83963;
XX	
DT	05-FEB-1999 (first entry)
XX	
DE	Recombinant human metFc-OB protein variant.
XX	
KW	Recombinant; metFc-OB protein; FC region; immunoglobulin; Ig; OB;
KW	obesity; human; adiposity; blood lipid; diabetes type II; insulin
KW	hypoglycaemic; antihypertensive; diuretic; appetite suppressant;
KW	suspension; variant.
XX	

OS	Homo sapiens.
XX	
PN	MO9846257 -A1.
XX	
PD	22-OCT-1998.
XX	
PF	16-APR-1998; 98WO-0507828.
XX	
PR	14-APR-1998; 98US-0059467.
PR	17-APR-1997; 97US-0843971.
XX	
PA	(AMGE-) AMGEN INC.
XX	
PI	Brems DN, French DL, Speed MA;
XX	
DR	WPI; 1998-594525/50.
XX	
DR	N-PSDB; V69686.
XX	
PT	Concentrated suspension of fusion of obesity protein with Fc
PT	immunoglobulin fragment - stable at physiological pH, used for e.g
PT	reduction of weight and blood lipid levels, and for treatment of
PT	type II diabetes

Claim 2; Fig 6A-C; 47pp; English.

This represents a recombinant metFc-OB protein variant which consists of an Fc region of human immunoglobulin (Ig) fused to a human OB (obesity) protein. The invention provides a human OB protein suspension that contains at least 0.5 mg/ml of the human OB protein derivatised by attachment of the Fc region of an Ig to the N-terminus of OB, and has a pH 6-8. The suspensions are used to reduce weight, adiposity and blood lipid levels, to treat or prevent diabetes type II, and to increase lean mass and insulin sensitivity. They may be used in conjunction with insulin, hypoglycaemics, antihyperemives, diuretics, appetite suppressants etc. These suspensions are stable and active at physiological pH and are ready-for-use formulations that do not require freezing or freeze drying. As they are very concentrated, only small volumes are required and they provide a sustained-release effect, with increased potency and reduced frequency of injection.

sq Sequence 374 AA;

query Match	55.1%;	Score 1238;	DB 19;	Length 374;
Best Local Similarity	100.0%;	Pred. No. 6.1e-76;		
Matches 228;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

Qy	1	MDKHHTOPBCAPELLGGSPSELPKPKOTLIMSRPEYTCVVVYDSDHPKFNMY	60
Db	1	mdkhttopcappelggspsefltpkpokdimstrepevtcavvdshdpevkfmwy	60
Qy	61	DGVEVHNNAKTRPEEOYNSTRVSVLTLYHODWLNGEKYCKVSNKALPAPIETKSKA	120
Db	61	dgvevhnaktprceqynstnyrvsvltvlhgdwlngkeyckrsknalpapektstka	120
Qy	121	KGQREPOVYTLPPSRBELTKNOVSLTCLYKGYPSDIAVEMWSNGOPENNKTTPVLD	180
Db	121	kgqrepevytlppsrbeltknqvsltclvkfygsdiaawesngpennkttppvld	180
Qy	181	SDGSFFLYSKTLVDKSMQOCNNVSCGVMEALJHNHTOKSLSLSPK	228
Db	181	sdgssfflysktlvdksrwqgnvscsvmealnhytlqslslspspk	228

RESULT	3
W49075	
ID	W49075 standard; Protein; 374 AA.
XX	
AC	W49075;
XX	
DT	18-NOV-1998 (first entry)
XX	
RE	Recombinant human MetFc-OB variant 2 protein

XX XX Recombinant human MetFc-OB variant 2 protein; chimeric; immunoglobulin;
KM high blood lipid level; arterial sclerosis; stroke; Fc-OB fusion protein;
KM diabetes.
XX XX
OS Homo sapiens.
OS Synthetic.
XX XX
FH Key Location/Qualifiers
FT Protein 2..374
FT /note= "Recombinant human Fc-OB variant 2 protein"
FT 229..374
FT Region /note= "human OB protein"
XX XX
XX WO9828427-A1.
XX XX
XX 02-JUL-1998.
XX XX
PD 11-DEC-1997; 97WO-US23183.
XX XX
PF 20-DEC-1996; 96GS-0770973.
PA (AMGE-) AMGEN INC.
XX XX
PI Hecht RI, Mann MB;
XX XX
DR WPI: 1998-377658/32.
DR N-PSDB: V32902.
XX XX
XX New fusion proteins of OB and Fc - used for treating e.g. excess
PT weight, diabetes, arterial sclerosis, arterial plaque, high blood
PT lipid level, gall stones or stroke
XX XX
XX Claim 2: Fig 5A-5C; 107pp; English.
XX XX
XX The present sequence represents a recombinant human MetFc-OB variant 2
CC fusion protein having a 5 residue deletion of residues 2-6 of the
CC wild-type Fc-OB protein sequence shown in W48073. The invention provides
CC Fc-OB fusion proteins whereby the Fc region of an immunoglobulin or its
CC analogue is linked, either directly or indirectly using a linker, to the
CC N-terminus of an OB protein or its analogue. The Fc-OB fusion proteins
CC are claimed to demonstrate increased stability and clearance rate and
CC decreased degradation as compared to OB protein or a fusion of Fc to
CC the C-terminus of the OB protein. These Fc-OB fusion proteins are also
CC claimed to be useful for treating excess weight in an individual or
CC animal or for treating co-morbidities associated with excess fat such as
CC diabetes, high blood lipid level, arterial sclerosis and stroke.
Sequence 374 AA:
Query Match 55.1%; Score 1238; DB 19; Length 374;
Best Local Similarity 100.0%; Pred. No. 6, 1e-76;
Matches 228; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MDKTHCPPCAPAPELLGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKRWIV 60
DB 1 mdkthcpcpapellggsvflfppkpkdtlmisrtpevtcvvdvshedpevkrmv 60
QY 61 DGVEVNAKTKPREEOYNSTRVSVTLVHODMLNGKCKVSNKALPAPTEKTSKA 120
DB 61 dgvevnahtkpreeqnstrvsvtlvhdwlnqkckvsnalpaplextlska 120
QY 121 KGPPEPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAEWESNGQPENNYTTTPVLD 180
DB 121 kgpprepgvtytlppsrdeltkngvsltlclvkgyfypsdiaweesngqpenytktpvld 180
QY 181 SDGSFELYSLTVDKSRWQGNVFCGVMAEALHNHTQKSLSLSPCK 228
DB 181 sdgsfelysltlvdksrwqgnvfscvmaealhnhtqgslslspck 228
RESULT 4

Y01372
ID Y01372 standard; Protein: 235 AA.
XX XX
AC Y01372:
XX XX
DT 04-JUN-1999 (first entry)
XX XX
DE Amino acid sequence of Fc fragment of human IgG.
XX XX
XX FcRn: binding; epithelial cell; immune system; modulation; antigen;
XX pathogen; autoimmune disease; allergen; tumour; therapeutic; cytokine;
XX chemotherapy agent; interferon; insulin; human growth hormone; fertility;
XX drug; calcitonin; steroid; immunity; mucosal; AIDS; hepatitis; Fc; human;
XX immunoglobulin; 196.
XX XX
OS Homo sapiens.
XX XX
FH Key Location/Qualifiers
FT Misc-difference 230
FT /note= "encoded by TGA"
XX XX
XX WO9304813-A1.
XX XX
XX 04-FEB-1999.
XX XX
PF 24-JUL-1998; 98WO-US15395.
XX XX
XX 24-JUL-1997; 97US-0899856.
XX XX
PA (BGMN) BRIGHAM & WOMENS HOSPITAL.
PA (UYBR-) UNIV BRANDEIS.
XX XX
PI Blumerg RS, Lencer WI, Simister NE;
XX XX
DR WPI: 1999-153297/13.
DR N-PSDB: X27800.
XX XX
PT Delivering therapeutics, particularly antigens to epithelial cells -
PT comprises use of a conjugate of the therapeutic and an FcRn binding
PT partner
XX XX
XX Disclosure: Fig 1; 74pp; English.
XX XX
XX The invention relates to methods of delivering molecules to a mammal by
CC administering a conjugative of a therapeutic or a bioactive substance,
CC and an FcRn binding partner targeted to epithelial cells expressing FcRn.
CC This can be used for modulating a mammalian immune system wherein, the
CC bioactive substance is an antigen characteristic of a pathogen of an
CC autoimmune disease, an allergen, or a tumour. The delivering method is
CC used to deliver therapeutics, including chemotherapy agents, cytokines
CC including interferon, hormones, including insulin and human growth
CC hormone, fertility drugs, calcitonin, calcitriol and other bioactive
CC steroids to intestinal, mucosal and lung epithelium. The method is also
CC used for trans epithelial delivery of antigens to provoke tolerance and
CC immunity. The method provides an immunisation, that specifically targets
CC the mucosal surfaces, and does not have the risks associated with
CC injections, including needle transmission of AIDS or hepatitis, of prior
CC art immunisation methods. The present sequence represents the amino acid
CC sequence of an Fc fragment of human immunoglobulin IgG.
XX XX
SQ Sequence 235 AA:
Query Match 55.1%; Score 1237; DB 20; Length 235;
Best Local Similarity 97.4%; Pred. No. 4, 1e-76;
Matches 228; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 1 MDKTHCPPCAPAPELLGGSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKRWIV 60
DB 2 vdkthcpcpapellggsvflfppkpkdtlmisrtpevtcvvdvshedpevkrmv 61
QY 61 DGVEVNAKTKPREEOYNSTRVSVTLVHODMLNGKCKVSNKALPAPTEKTSKA 120
DB 1 dgvevnahtkpreeqnstrvsvtlvhdwlnqkckvsnalpaplextlska 120

Db 62 gvevhnaktkpreegynsttyrvsvltvlnqdwlngkeyckvsnkalpapietktska 121
 QY 121 KGPREPVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMWESNGOPENNYKTTTPVLD 180
 Db 122 kgqprepvylppsrdeitknqvsitclvkgfypsdiawesngqpennykttppvld 181
 QY 181 SDGSFELYSKLTVDKSRWQGNVFSQSYMHEALNNHTOKSLSPGKETPPK 234
 Db 182 sdgsfelyskltvdksrtwgggnvicsymhealnnhytqkslspgkxxvrrpr 235

RESULT 5
 W26649
 ID W26649 standard; Protein; 651 AA.
 AC W26649;
 XX
 DT 12-FEB-1998 (first entry)
 Chimeric receptor hCTM01/G1/zeta.

KW Cell activation; chimeric receptor; DNA delivery; CTM01; scfv;
 KW IgG1; T cell receptor zeta chain; cell proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.

XX Chimeric - Homo sapiens.
 OS
 PN W09723613-A2.
 PD 03-JUL-1997.
 XX
 PF 23-DEC-1996; 96MO-GB03209.
 XX
 PR 21-DEC-1995; 95GB-0026131.
 XX
 PA (CLLT) CELLTech THERAPEUTICS LTD.
 XX
 PI Babbington CR, Flinney HM, Lawson ADG, Weir ANC;
 XX
 DR WPI: 1997-351052/32.
 DR N-PDB: T90512.
 XX
 XX New DNA systems for activating cells - comprising DNA coding for a
 chimeric receptor comprising 2 or more different cytoplasmic
 signalling components.
 XX
 PS Disclosure: Fig 7; 90pp; English.

CC This protein comprises a chimeric receptor consisting of an scfv
 CC engineered from anti-CD3 human antibody CTM01 linked to an
 CC extracellular spacer comprising the human IgG1 hinge, CH2 and CH3,
 CC linked to transmembrane and intracellular regions of the human T
 CC cell receptor zeta chain. It can be expressed in host cells (e.g.
 CC Jurkat) using a chimeric receptor gene (see T90512) constructed
 CC from DNA cassettes encoding each receptor component. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/idiopathic disease (claimed).

CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease, or diabetes (claimed).

SO Sequence 651 AA;
 Query Match 55.1%; Score 1236.5; DB 18; Length 651;
 Best Local Similarity 62.6%; Pred. No. 1.5e-75;
 Matches 258; Conservative 18; Mismatches 61; Indels 75; Gaps 9;

QY 2 DKHTGCPCPAPPELLGSPVFLPPPKKDTLMSRPEVTCVYVDVSHPEPVKFNMYVD 61
 Db 288 dkhtgcpcpapelllgpsvflfppkdtlmsrpevcvvdvshpepvkfnmyvd 347
 QY 62 GVEVHNKTKPREQYNSTYRVSVTLVHQMUNGKEYCKVSNKALPAPIETKTSKAK 121
 Db 348 gvevhnaktkpreegynsttyrvsvltvlnqdwlngkeyckvsnkalpapietktska 407
 QY 122 GQPREPVYTLPPSRDELTKNOVSLTCLVKGFPSPDIAMWESNGOPENNYKTTTPVLD 181
 Db 408 gqprepvylppsrdeitknqvsitclvkgfypsdiawesngqpennykttppvld 467
 QY 182 DGSFELYSKLTVDKSRWQGNVFSQSYMHEALNNHTOKSLSPGKETPPKRYLHAYDEE 241
 Db 468 dgsfelyskltvdksrtwgggnvicsymhealnnhytqkslspgk-ldpk----- 518
 QY 242 TSHQLCDKCPPTYLKQCTAKKTKVCAPCPDHYTDSWHTDECLYCSYCKEQLYVK 301
 Db 519 ----lc-----yldgllfflygvalitalflr 540
 QY 302 -----QECNRHNRVCECKEGRYLEIEPOLKHRSCPPGCVVQAGTPERNYV 348
 Db 541 vkfesaadapayqggnqlynn--elnlgreeydvldkrrgrdpemg----gkpr---- 590
 QY 349 CKRCPDGFSENETSKRKPCKRHTNCSVFGLLTQKGNATHDNCSGNSESTQ 400
 Db 591 -knpgegly-nelqkdkmaeyseigmkgerrrxg--hdglyglstac 637

RESULT 6
 W26650
 ID W26650 standard; Protein; 692 AA.
 AC W26650;
 XX
 DT 12-FEB-1998 (first entry)
 XX
 DE Chimeric receptor hCTM01/G1/zeta-CD28.

KW Cell activation; chimeric receptor; DNA delivery; CTM01; scfv;
 KW IgG1; CD28; T cell receptor zeta chain; proliferation; cytokine;
 KW inflammation; effector; cell differentiation; antibody secretion;
 KW phagocytosis; tumour infiltration; adhesion; infection; cancer;
 KW allergy; rheumatoid arthritis; osteoarthritis; asthma; eczema;
 KW inflammatory bowel disease; cystic fibrosis; sickle cell anaemia;
 KW psoriasis; multiple sclerosis; transplant rejection; diabetes;
 KW graft versus host disease; human; therapy.

XX Chimeric - Homo sapiens.
 OS
 PN W09723613-A2.
 PD 03-JUL-1997.
 XX
 PF 23-DEC-1996; 96MO-GB03209.
 XX
 PR 21-DEC-1995; 95GB-0026131.
 XX
 PA (CLLT) CELLTech THERAPEUTICS LTD.

PI Bebbington CR, Flinney HM, Lawson ADG, Weir ANC;
 XX WPI: 1997-351052/32.
 DR N-PSDB; T90513.
 XX
 PT New DNA systems for activating cells - comprising DNA coding for a
 PT chimeric receptor comprising 2 or more different cytoplasmic
 PT signalling components.
 PS Disclosure: Fig 8; 90pp; English.
 XX
 CC This protein comprises a chimeric receptor consisting of an scfv
 CC engineered from anti-CD3 human antibody C7M01 linked to an
 CC extracellular spacer comprising the Human IgG1 hinge, CH2 and CH3,
 CC linked to the Transmembrane and Intracellular components of the
 CC human T cell receptor zeta chain, fused to the intracellular region
 CC of human CD28. It can be expressed in host cells (e.g. Jurkat)
 CC using a chimeric receptor gene (see T90513) constructed from DNA
 CC cassettes encoding each component of the receptor. In a claimed
 CC cell activation process an effector cell is transformed with DNA
 CC encoding a chimeric receptor containing 2 or more different
 CC cytoplasmic signalling components. Also claimed is use of DNA
 CC encoding a recombinant chimeric receptor in a DNA delivery system.
 CC The DNA delivery systems can be used for the activation of cells to
 CC provide e.g. an increase in cell proliferation, expression of
 CC cytokines with e.g. pro- or anti-inflammatory responses, stimulation
 CC of cytolytic activity, differentiation or other effector functions,
 CC antibody secretion, phagocytosis, tumour infiltration and/or
 CC increased adhesion. They can be used in the treatment of e.g.
 CC infectious disease, inflammatory disease, cancer, allergic/atopic
 CC disease, congenital disease, dermatologic disease, neurologic
 CC disease, transplants and metabolic/adipopathic disease (claimed).
 CC In particular, they can be used in the treatment of rheumatoid
 CC arthritis, osteoarthritis, inflammatory bowel disease, asthma,
 CC eczema, cystic fibrosis, sickle cell anaemia, psoriasis, multiple
 CC sclerosis, organ or tissue transplant rejection, graft-versus-host
 CC disease or diabetes (claimed).
 CC
 XX Sequence 692 AA:
 SQ

Query Match 55.1%; Score 1236.5; DB 18; Length 692;
 Best Local Similarity 62.6%; Pred. No. 1.6e-75;
 Matches 258; Conservative 18; Mismatches 61; Indels 75; Gaps 9;

QY 2 DKHTHCPCPAPPELLGSPVLEFPKPKDTLMSRPEVTCVVVDSHEDPEVKFNMYVD 61
 DB |||||||
 DB 288 dkhtcpcpapellgspvflfppkpkdtlmsrtpcvvvdshedpevkfnmyvd 347
 DB 62 GVEYHNAKTPREQYVSTRVSVLTVLHODVLNGEKYCKVSNKALPAPIETISKAK 121
 DB gvevhnaktpreeqvstryvsvltvlhqdvlngkyckvsnkalpapietiskak 407
 DB 122 GQREPOVYTRPSRDELTKNOVSLTGLVGFSPDRAVENESGQENNYKTPPYLDS 181
 DB |||||||
 DB 408 gqreppvytrpsremtknqvslclvngfypsdlavewesgqepennyktppylids 467
 QY 182 DGSFFLYSKLTVDKSRMQQNVSCSYVMEALNNHYTQKSLSPGKETPPKTYLHDEE 241
 DB |||||||
 DB 468 dgsfflyskltvdksvrvgqnvfscvmealhnhyqkalslspgk--ldpk----- 518
 QY 242 TSHQLCDKCPPTGYLKQCTAKKTYCACPDPHYTRDSNHTSECLCYSPVCKELOLYK 301
 DB |||||
 DB 519 ----lc-----yldgllfygvlltalflr 540
 QY 302 -----QECNRTHNRCVCECKGRYLEIEFCLKHSRCPGPGVVQAGTPERNTV 348
 DB |||||
 DB 541 vkfsrsadapaygqgqqln---elnlgrreydvldkrrgrdpeng-----gkpr--- 590
 QY 349 CKRCPDGFSENETSSKAPCKRHTNCSVGLLLRQGNATHDNICSGNSESTQ 400
 DB |||||
 DB 591 -knpqegily-nelqkdkmaeayseigmkgerrirgk--hdgilygststak 637

RESULT 7
 R27163
 ID R27163 standard; Protein; 347 AA.
 XX
 AC R27163;
 XX
 DT 20-MAY-1998 (first entry)
 XX
 DE CD2 binding LFA-3-Ig fusion protein.
 XX
 KW Lymphocyte associated antigen-3; T-lymphocyte accessory molecule;
 KW deletion mutant; CD2 binding site; immunomodulator; immunoglobulin;
 KW preLFA3TIP; LFA-3(92)IgG; pSAB152; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT peptide 1..28
 FT /label= LFA-3-signal
 FT region 29..120
 FT /label= LFA-3-aminoacids_1-92
 FT region 121..130
 FT /label= IgG1_hinge
 FT domain 131..239
 FT /label= IgG1_CH2
 FT domain 240..347
 FT /label= IgG1_CH3
 XX
 PN EP503648-A.
 XX
 PD 16-SEP-1992.
 XX
 PF 12-MAR-1992; 92EP-0104320.
 XX
 PR 12-MAR-1991; 91US-0667971.
 PR 07-OCT-1991; 91US-0770967.
 XX
 PA (BIO) BIOGEN INC.
 XX
 PI Miller GT, Rosa MD, Wallner BP;
 XX
 DR WPI: 1992-309760/38.
 DR N-PSDB; Q28684.
 XX
 XX CD2-binding domain of lymphocyte function associated antigen-3
 PT and DNA .. for diagnosing and treating inflammation and
 PT autoimmune diseases, e.g. systemic lupus erythematosus and
 PT rheumatoid arthritis
 XX
 PS Claim 13; Fig 12; 85pp; English.
 XX
 CC The plasmid pSAB152 contains the DNA sequence encoding the LFA-3
 CC signal sequence, the amino terminal 92 amino acids of mature LFA-3,
 CC ten amino acids of the hinge region of IgG1 and the CH2 and CH3
 CC constant domains of IgG1 (see Q28678-9 and Q28681-2 for details of
 CC the construction of pSAB152). A NotI fragment containing the coding
 CC sequence of pSAB152 was used in the construction of expression
 CC vector pMDR(92)Ig-3 which can be stably maintained in CHO cells to
 CC achieve continuous expression of LFA3TIP. The fusion protein can
 CC bind to CD2 and inhibit T cell activation, making it useful to
 CC treat acute and chronic inflammation, autoimmune disease and
 CC in immunomodulation.
 CC
 XX Sequence 347 AA:
 SQ

Query Match 54.9%; Score 1234; DB 13; Length 347;
 Best Local Similarity 99.6%; Pred. No. 1e-75;
 Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 MDKTHNCPAPPELLGSPVLEFPKPKDTLMSRPEVTCVVVDSHEDPEVKFNMYVD 60
 |||||||

Dh 120 vdkhtcpcpapellggpsvflfpkpkdtlmistrpevcvvvdshedpevkfmvy 179
Qy 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODWLNKEKCKKSNKALPAPIETKISK 120
Dh 180 dgevhnaaktpreeqynstyyvsvltvlhqdwlngkeyckvsnkalpapietkiska 239
Qy 121 KGOPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
Dh 240 kgqprepgvyltpprdelatknqvsiltclvkgfypsdlavewesngqpennyktcpvld 299
Qy 181 SDGSFFLSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPK 228
Dh 300 sdgsfflyskltvdksrtwggnvfscsymhealhnhytqkslsispk 347
RESULT 8
ID Y83136 standard; Protein: 347 AA.
Y83136:
24-JUL-2000 (first entry)
Huhan transmembrane LFA-3/1gG fusion protein LFA3rip.
LFA3: CD2: cell signalling; modulation; lymphocyte; T cell;
memory effector T lymphocyte; psoriatic arthritis;
rheumatoid arthritis; multiple sclerosis; atopic dermatitis;
uveitis; inflammatory bowel disease; Crohn's disease;
ulcerative colitis; cutaneous T cell lymphoma; inhibition; treatment;
therapy.
Homo sapiens.
MO200012113-A2.
09-MAR-2000.
31-AUG-1999; 99MO-US20026.
31-AUG-1998; 98US-0098456.
(BIOJ) BIOGEN INC.
Magilavy D;
WPI: 2000-282928/24.
N-PSDB: 293401.
PT Selective modulation of memory effector T lymphocytes by administration
PT of a CD2 binding agent which inhibits the CD2/LFA-3 interaction useful
PT for treating conditions such as inflammatory bowel diseases, psoriatic
PT arthritis
PS Disclosure; Page 75-76; 76pp; English.
XX Modulation of LFA3/CD2 interaction by administration of a CD2 binding
CC agent inhibits CD2 signalling and T cell proliferation and activation
CC and more particularly modulates the number and/or distribution of
CC memory effector T lymphocytes. The method can be used for treating a
CC condition in a subject where the condition is characterized by memory
CC effector T lymphocytes playing a role in the pathogenesis of the
CC condition such as psoriatic arthritis, rheumatoid arthritis,
CC multiple sclerosis, atopic dermatitis, uveitis, inflammatory bowel
CC disease, Crohn's disease, ulcerative colitis and cutaneous T cell
CC lymphoma and where the method comprises administering to the subject
CC an amount of CD2 binding agent sufficient to modulate the memory
CC effector T lymphocytes. The methods provide inhibition of antigen
CC specific interactions for all antigens present, inhibition of T cell
CC activation, no general immunosuppression, and possibly induction of
CC tolerance.
XX Sequence 347 AA;
SQ

Query Match 54.98; Score 1234; DB 21; Length 347;
Best Local Similarity 99.68; Pred. No. 1e-73;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MDKHTCPCPAPELLGSPVFLFPKPKDTLMISRPPEVTCVVVDVSHEDPEVKFMVY 60
Dh 120 vdkhtcpcpapellggpsvflfpkpkdtlmistrpevcvvvdshedpevkfmvy 179
Qy 61 DGEVHNAKTRPREQYNSTRVSVLTVLHODWLNKEKCKKSNKALPAPIETKISK 120
Dh 180 dgevhnaaktpreeqynstyyvsvltvlhqdwlngkeyckvsnkalpapietkiska 239
Qy 121 KGOPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVWESNGQPENNYKTPPVLD 180
Dh 240 kgqprepgvyltpprdelatknqvsiltclvkgfypsdlavewesngqpennyktcpvld 299
Qy 181 SDGSFFLSKLTVDKSRMOQGNVFCSCVMHEALHNHYTQKSLSLSPK 228
Dh 300 sdgsfflyskltvdksrtwggnvfscsymhealhnhytqkslsispk 347
RESULT 9
ID W73513 standard; Protein: 388 AA.
W73513:
AC W73513;
DT 02-MAR-1999 (first entry)
XX Rabbit TGFbetarII:Fc protein.
DE Transforming growth factor-beta receptor; TGF-beta receptor; arthritis;
XX fusion protein; fibroproliferative disorder; diabetic nephropathy;
KW glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;
KW collagen vascular disorder; therapy; rabbit.
XX Oryctolagus sp.
OS WO9848024-A1.
XX 29-OCT-1998.
PD 16-APR-1998; 98MO-US07587.
XX 18-APR-1997; 97US-0044641.
PR (BIOJ) BIOGEN INC.
XX Cate R, Gotwals P, Koteliarsky V, Sanicola-Nadel M;
PI WPI: 1998-609994/51.
XX N-PSDB: V08998.
DR Transforming growth factor-beta receptor fusion protein - used to
PT treat fibroproliferative disorders
PT Claim 4; Page 18-19; 70pp; English.
XX This sequence is a fusion protein of the rabbit transforming growth
CC factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The
CC encoded protein is an example of a protein of the invention, which are
CC isolated TGF-beta receptor fusion proteins that competitively inhibit
CC binding of TGF-beta to TGF-beta receptor. The fusion protein can be used
CC in a method for lowering the levels of TGF-beta in an individual having
CC arthritis. It can also be used to treat medical conditions such as a
CC fibroproliferative disorders. The fibroproliferative disorder is a
CC kidney, intraocular or pulmonary fibrosis, especially selected from
CC diabetic nephropathy, glomerulonephritis, proliferative
CC vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used
CC to treat collagen vascular disorders, including systemic sclerosis,
CC polymyositis, scleroderma, dermatomyositis, and systemic lupus

CC erythematous. They can also be administered following coronary
CC angioplasty, to prevent restenosis or scarring and reclosing of arteries.
XX
SQ Sequence 388 AA:

Query Match 54.9%; Score 1234; DB 19; Length 388;
Best Local Similarity 99.6%; Pred. No. 1.2e-75;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKHTCPCPAPABELIGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNTV 60
Db 161 vdkthcpcpapel1lgpsvflfpkpkdltmistrpctcvvdshdpvkvfntv 220
OY 61 DGEVHNATKPREBOYNSTRVSVLTVLHODMLNGKREYKCKVSNKALPAPLEKTIKSA 120
Db 221 dgevhnahtkpreegynstlyrvsvltvlhgdwlngkeykckvsnkalpaplektiska 280
OY 121 KGPPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 180
281 kgpprepvytlppsrdeltknqvslclvkgyfspdlaivesngqpennnyktppvld 340
OY 181 SDGSFELYSKLTVDKSRMOQGNFSCSVHMEALHNHYTKSLSPGK 228
Db 341 sdgsfelyskltvdksrmoqgnvfscsvhmealhnhytkslspsgk 388

RESULT 10
W73514
ID W73514 standard; Protein: 388 AA.

XX W73514:

DT 02-MAR-1999 (first entry)

XX Human TGFbetaRII:Fc protein sequence.

DE Transforming growth factor-beta receptor; TGF-beta receptor; arthritis;

KW fusion protein; fibroproliferative disorder; diabetic nephropathy;

KM glomerulonephritis; proliferative vitreoretinopathy; myelofibrosis;

KW collagen vascular disorder; therapy; human.

OS Homo sapiens.

XX W09848024-A1.

XX 29-OCT-1998.

XX 16-APR-1998; 98WO-US07587.

XX 18-APR-1997; 97US-0044641.

XX (BIOJ) BIOGEN INC.

XX Cate R, Gotwals P, Koteliansky V, Sanicola-Nadel M;

XX WPI: 1998-609994/51.

XX N-PSDB: V08999.

XX Transforming growth factor-beta receptor fusion protein - used to

XX treat fibroproliferative disorders

XX Claim 4; Page 19-20; 70pp; English.

XX This sequence is a fusion protein of the human transforming growth
CC factor-beta receptor II (TGF-betaRII) and an antibody Fc region. The
CC encoded protein is an example of a protein of the invention, which are
CC isolated TGF-beta receptor fusion proteins that competitively inhibit
CC binding of TGF-beta to TGF-beta receptor. The fusion protein can be used
CC in a method for lowering the levels of TGF-beta in an individual having
CC arthritis. It can also be used to treat medical conditions such as
CC fibroproliferative disorders. The fibroproliferative disorder is a
CC kidney, intraocular or pulmonary fibrosis, especially selected from

CC diabetic nephropathy, glomerulonephritis, proliferative
CC vitreoretinopathy, or myelofibrosis. The fusion proteins can also be used
CC to treat collagen vascular disorders, including systemic sclerosis,
CC polymyositis, scleroderma, dermatomyositis, and systemic lupus
CC erythematous. They can also be administered following coronary
CC angioplasty, to prevent restenosis or scarring and reclosing of arteries.
XX
SQ Sequence 388 AA:

Query Match 54.9%; Score 1234; DB 19; Length 388;
Best Local Similarity 99.6%; Pred. No. 1.2e-75;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 1 MDKHTCPCPAPABELIGSVFLFPKPKDLMISRTPEVTCVVDVSHEDPEVKFNTV 60
Db 161 vdkthcpcpapel1lgpsvflfpkpkdltmistrpctcvvdshdpvkvfntv 220
OY 61 DGEVHNATKPREBOYNSTRVSVLTVLHODMLNGKREYKCKVSNKALPAPLEKTIKSA 120
Db 221 dgevhnahtkpreegynstlyrvsvltvlhgdwlngkeykckvsnkalpaplektiska 280
OY 121 KGPPEPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEMESNGQPENNYKTTPPVLD 180
281 kgpprepvytlppsrdeltknqvslclvkgyfspdlaivesngqpennnyktppvld 340
OY 181 SDGSFELYSKLTVDKSRMOQGNFSCSVHMEALHNHYTKSLSPGK 228
Db 341 sdgsfelyskltvdksrmoqgnvfscsvhmealhnhytkslspsgk 388

RESULT 11
Y54063
ID Y54063 standard; Protein: 388 AA.

XX Y54063:

DT 27-MAR-2000 (first entry)

DE Amino acid sequence of TGF-beta type II receptor variant/IgG1 fusion.

DE Splice variant; rabbit; transforming growth factor-beta; TGF-beta;

KW type II receptor; Fc portion; human IgG1; fusion protein; arthritis;

KW fibroproliferative disease; renal; intra-ocular; pulmonary; fibrosis;

KW diabetic nephropathy; glomerulonephritis; collagen vascular disease;

KW proliferative vitreoretinopathy; myelofibrosis; systemic sclerosis;

KW polymyositis; scleroderma; dermatomyositis; systemic lupus erythematous;

KW restenosis; wound; connective tissue production; adhesion; scarring;

KW post-radiation fibrosis.

XX Synthetic.

XX Oryctolagus cuniculus.

XX Homo sapiens.

XX W09965948-A1.

XX 23-DEC-1999.

XX 16-JUN-1999; 99WO-US13629.

XX 16-JUN-1998; 98US-0089452.

XX (BIOJ) BIOGEN INC.

XX Koteliansky V, Gotwals P, Cate R, Sanicola-Nadel M;

XX WPI: 2000-106083/09.

XX N-PSDB: Z45251, Z45252.

XX New fusion protein of a splice variant of transforming growth

XX factor-beta receptor, for inhibiting the growth factor, e.g. in

XX treatment of fibrosis

multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; mouse; IgG2a Fc domain.

Chimeric - Homo sapiens.
Chimeric - Mus sp.

Key Location/Qualifiers
1..166
/label= natural_human_IFN-beta-1a
167..171
/label= Enterokinase_linker
172..399
Region /label= Mouse IgG2a-Fc portion
/note= "comprises the hinge region, CH2 and CH3 constant domains of mouse Ig"

WO200023472-A2.

27-APR-2000.

15-OCT-1999; 99WO-US24200.

16-OCT-1998; 98US-0104491.

16-FEB-1999; 99US-0120237.

(BIOI) BIOGEN INC.

Whitty A, Runkel L, Brickelmaier M, Hochman P;

WPI: 2000-339654/29.

N-PSDB; D00166.

Fusion proteins comprising interferon-beta-1a useful for inhibiting angiogenesis -

Example 2; Fig 2; 82pp; English.

The patent discloses fusion proteins comprising glycosylated interferon-beta (IFN-beta) especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein that consists of mature human IFN-beta-1a and mouse IgG2a Fc domain separated by an enterokinase linker. The fusion protein is useful for inhibiting angiogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by neovascularisation.

Sequence 399 AA:

Query Match 54.9%; Score 1234; DB 21; Length 399;

Best Local Similarity 99.6%; Pred. No. 1.2e-75; Mismatches 0; Indels 0; Gaps 0;

Matches 227; Conservative 1;

1 MDKTHCCPCPAEELGSPVFLPPKPKDTLMISRPETVCVVDVSHEDPEVKRMVY 60
:|||||
172 vdkthccpcpapel1g9psvflfppkpkdtlmisrpetcvvdvshedpevkrmv 231
61 DGEVHNATKPREEOYNSTRVAVSLTVLHOMLNGKEKCKVSNKALPAPLEKITSKA 120
:|||||
232 dgevhnatkpreeqynstrvavsltlvldhmlngkekcvcvsnkalpapektiska 291
121 KGQPREPQVYTLPPSRDELTKNOVSLTCLVKGFPSPSDIAVWESNGQPENNYKTPPEVID 180
:|||||
292 kgqprepyvtylppsrde1tkngvsltc1vkfgfypsdiawesngqpenyktppvid 351
181 SSGSFLYSKLTVDKSRMOGNFSSVMEALHNHYTQSLSPGK 228
:|||||
352 ssgsflyskltvdksrmoqnfssvmealhnhytqslspgk 399

RESULT 14

Y70868
ID Y70868 standard; Protein: 418 AA.

AC Y70868;

31-JUL-2000 (first entry)

Human interferon-beta-1a G162C-IgG1 Fc direct fusion protein.

Human; interferon-beta-1a; IFN-beta-1a; immunoglobulin; fusion protein; angiogenesis; antisclerotic; antiinflammatory; immunosuppressive; cancer; cytostatic; virocidic; hepatotropic; antiangiogenic; treatment; fibrosis; multiple sclerosis; inflammatory disease; autoimmune disease; hepatitis; viral infection; neovascularisation; IgG1 Fc domain; VCAM-1; mutant; vascular cell adhesion molecule-1.

Homo sapiens.

Synthetic.

Key

Peptide

Protein

Misc-difference 186

/note= "Wild type IFN-beta-1a gly at position 162 is substituted by Cys"

Region /label= Human_IgG1-Fc portion

/note= "comprises hinge, CH2 and CH3 domains of IgG1 heavy chain"

WO200023472-A2.

27-APR-2000.

15-OCT-1999; 99WO-US24200.

16-OCT-1998; 98US-0104491.

16-FEB-1999; 99US-0120237.

(BIOI) BIOGEN INC.

Whitty A, Runkel L, Brickelmaier M, Hochman P;

WPI: 2000-339654/29.

N-PSDB; D00167.

Fusion proteins comprising interferon-beta-1a useful for inhibiting angiogenesis -

Example 5; Fig 10; 82pp; English.

The patent discloses fusion proteins comprising glycosylated interferon-beta (IFN-beta) especially an immunoglobulin (Ig) protein. The present sequence is a fusion protein consisting of a vascular cell adhesion molecule-1 (VCAM-1) signal sequence, a modified human IFN-beta-1a and human IgG1 Fc domain, which are directly fused without a linker sequence. The fusion protein is useful for inhibiting angiogenesis in a patient. It may also be used to treat multiple sclerosis, fibrosis, inflammatory and autoimmune diseases, cancers, hepatitis and viral infection characterised by neovascularisation.

Sequence 418 AA:

Query Match 54.9%; Score 1234; DB 21; Length 418;
Best Local Similarity 99.6%; Pred. No. 1.3e-75;
Matches 227; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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